

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2005, 18:53:39 ; Search time 89.1987 Seconds
(without alignments)
1049.298 Million cell updates/sec

Title: US-10-695-980-32

Perfect score: 1341

Sequence: 1 MSAAHLPKADLTATSLIVSG.....LHPTVPMWRLPSTRKGDPA 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp19808:***
2: geneseqp19908:***
3: geneseqp20008:***
4: geneseqp20018:***
5: geneseqp20028:***
6: geneseqp20038:***
7: geneseqp20038:***
8: geneseqp20048:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1341	100.0	242	2	AAW69535
2	1341	100.0	242	6	ABU97244
3	1341	99.3	242	8	AD061161
4	1332	99.3	242	8	AD061078
5	1332	99.3	242	8	ADQ38247
6	1332	99.3	242	8	ADQ38247
7	1332	99.3	242	8	ADQ38247
8	1332	99.3	242	7	ADQ38247
9	1331	99.3	242	2	AAW62260
10	1331	99.3	242	8	AD061157
11	1331	99.3	242	8	AD061074
12	1331	99.3	242	8	ADQ38243
13	1331	99.3	242	8	ADQ38243
14	1331	99.3	242	8	ADQ38243
15	1336	98.9	299	5	AAW81818
16	1336	98.9	299	5	AAW81818
17	1180	88.0	212	2	AAW79058
18	1180	88.0	212	2	AAW79058
19	1044	77.9	242	2	AAW79058
20	1044	77.9	242	2	AAW79058
21	1044	77.9	242	2	AAW79058
22	1044	77.9	242	8	AD061159
23	1044	77.9	242	8	AD061159
24	1044	77.9	242	8	ADQ38245
25	1044	77.9	242	8	ADQ38245

26	1044	77.9	242	8	ADQ38240
27	600	44.7	258	8	AD061165
28	600	44.7	258	8	AD061082
29	600	44.7	258	8	ADQ38251
30	600	44.7	258	8	ADQ38251
31	600	44.7	258	8	ADQ38251
32	564	42.1	244	6	AAO16024
33	418.5	31.2	262	8	ADP74108
34	418.5	31.0	262	8	ADP74102
35	415.5	31.0	262	8	ADQ38319
36	415.5	31.0	262	8	ADQ94520
37	415.5	31.0	262	8	ADQ38370
38	415.5	31.0	262	8	ADQ38350
39	413.5	30.8	262	8	ADP74106
40	407.5	30.4	258	8	ADQ61167
41	407.5	30.4	258	8	ADQ61167
42	407.5	30.4	258	8	ADP74100
43	407.5	30.4	258	8	ADQ38253
44	407.5	30.4	258	8	ADQ38253
45	407.5	30.4	258	8	ADQ38253

ALIGNMENTS

RESULT 1

AAW69535 standard; protein; 242 AA.

AAW69535; 10-ANG-1999 (first entry)

crw2396 gene product beta-carotene beta-oxygenase.
Carotenoid; pigment; canthaxanthin; R1534; crtB; prephytyene synthase;
crtI; phytoene desaturase; crtI; lycopen cyclase; crtW2396;
beta-carotene beta-oxygenase; food product; fermentation.

Flavobacterium sp.

JP10155497-A.

16-JUN-1998.

02-DEC-1997; 97JP-00348653.

02-DEC-1996; 96EP-00810839.

(HOF) HOFFMANN LA ROCHE & CO AG F.

WPI; 1998-391048/34.

N-PSDB; AAV40147.

Preparation of carotenoid - comprises fermentation with transformed cell.

Claim 1; Fig 62; 80pp; Japanese.

The invention describes the preparation of carotenoid pigments e.g. canthaxanthin using a cell transformed by a vector having DNA sequences (a) to (e) or substantially homologous sequences. (a) a DNA sequence (crtB) coding for prephytyene synthase of Flavobacterium sp. R1534; (b) a DNA sequence (crtI) coding for phytoene desaturase of Flavobacterium sp. R1534; (c) a DNA sequence (crtI) coding for phytoene desaturase of Flavobacterium sp. R1534; (d) a DNA sequence (crtI) coding for phytoene desaturase of Flavobacterium sp. R1534; and (e) a DNA sequence (crtW2396) coding for beta-carotene beta-oxygenase of a microbe E-396 (FERM BP-4283). The carotenoid or a carotenoid mixture can also be used in preparation of food products. The method is an improved method of fermentation for carotenoid production.

Sequence 242 AA;

Query Match 100.0%; Score 1341; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 4.5e-143;
 Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAAHLPRKADLTATSLIVSGGIIAAMLALHVALWFLDAAHPILAVANFLGLTWLSVGL 60
 |||||
 DB 1 MSAAHLPRKADLTATSLIVSGGIIAAMLALHVALWFLDAAHPILAVANFLGLTWLSVGL 60

QY 61 FIITADHMGSVVPGPRANAMGOLVLMVYAGFSWRKKIVKMAHHRAGTDDDDPFH 120
 |||||
 DB 61 FIITADHMGSVVPGPRANAMGOLVLMVYAGFSWRKKIVKMAHHRAGTDDDDPFH 120

QY 121 GGPVRWYARFICTYFGMRGELLPIVITYYALMLGDRMWYVFWPLPSIIASIQLFVFGI 180
 |||||
 DB 121 GGPVRWYARFICTYFGMRGELLPIVITYYALMLGDRMWYVFWPLPSIIASIQLFVFGI 180

QY 181 WLPHRPGHDAPDRRNAASSRISDPVSLTCTHFGGYHHEHHLHPTVPMWRLPSTRTKGD 240
 |||||
 DB 181 WLPHRPGHDAPDRRNAASSRISDPVSLTCTHFGGYHHEHHLHPTVPMWRLPSTRTKGD 240

QY 241 TA 242
 |||||
 DB 241 TA 242

RESULT 2
 ABU97244
 ID ABU97244 standard; protein; 242 AA.

AC ABU97244;
 XX
 DT 28-JUL-2003 (first entry)
 XX
 DE Enzyme polypeptide #10.
 XX
 KM Enzyme; hydroxymethylglutaryl coenzyme-A reductase; HMGCoA reductase;
 KM isopentenyl diphosphate isomerase; HMGCoA synthase; mevalonate kinase;
 KM phosphomevalonate kinase; diphosphomevalonate decarboxylase; phyloene;
 KM carotenoid-producing cell; isoprenoid compound; fpp synthase; lycopen;
 KM farneyl diphosphate synthase; carotenoid; beta-carotene; zeaxanthin;
 KM canthaxanthin; astaxanthin; adonixanthin; cryptoxanthin; echinenone;
 KM adonitubin; C-4-isoprenoid compound; nutritional supplement;
 KM food colourant; animal feed pigment.
 XX
 XX Paracoccus carotinifaciens.
 OS
 XX
 PN WO200299095-A2.
 XX
 PD 12-DEC-2002.
 XX
 PF 05-JUN-2002; 2002WO-EP006171.
 XX
 PR 06-JUN-2001; 2001US-0296299P.
 XX
 XX (HOFF) ROCHE VITAMINS AG.
 PA
 XX
 PI Berry A, Bretzel W, Huemelin M, Lopez-Ulibarri R, Mayer AF;
 PI Yeliseev A;
 PI
 DR WPI; 2003-156856/15.
 DR N-PSDB; ACA99471.
 XX
 PT New isolated polypeptide used for isoprenoid production, includes amino
 PT acid sequence having e.g. mevalonate kinase, phosphomevalonate kinase or
 PT diphosphomevalonate decarboxylase activity.
 XX
 XX Example 12; Page 295-297; 307pp; English.
 PS
 XX
 CC The invention relates to an isolated polypeptide having the activity of
 CC an enzyme such as hydroxymethylglutaryl Coenzyme-A (HMGCoA) reductase,
 CC isopentenyl diphosphate isomerase, HMGCoA synthase, mevalonate kinase,
 CC phosphomevalonate kinase or diphosphomevalonate decarboxylase. The
 CC invention also relates to the production of a carotenoid-producing cell

CC and engineering a bacterium to produce an isoprenoid compound, comprising
 CC culturing a parent bacterium in a medium permitting expression of an
 CC isoprenoid compound and selecting a mutant bacterium from the culture
 CC medium that produces 1.1-1000 times more isoprenoid compound than the
 CC parent bacterium, introducing an expression vector comprising a farneyl
 CC diphosphate (fpp) synthase DNA fragment operably linked to an expression
 CC control sequence into the mutant bacterium, and selecting a bacterium
 CC that contains the expression vector and produces at least 1.1 times more
 CC isoprenoid compound than the selected mutant. The cell is useful for
 CC producing a carotenoid (phyloene, lycopen, beta-carotene, zeaxanthin,
 CC canthaxanthin, astaxanthin, adonixanthin, cryptoxanthin, echinenone or
 CC adonitubin) by culturing the cell under conditions permitting expression
 CC of the polypeptide encoded by the polynucleotide sequence and isolating
 CC the carotenoid from the cell or the medium of the cell. The carotenoids
 CC (C-4- isoprenoid compounds) are used as nutritional supplements,
 CC pharmaceuticals, food colourants and pigments for animal feeds. This
 CC sequence represents a polypeptide of the invention

QY Sequence 242 AA;
 XX
 SQ

Query Match 100.0%; Score 1341; DB 6; Length 242;
 Best Local Similarity 100.0%; Pred. No. 4.5e-143;
 Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAAHLPRKADLTATSLIVSGGIIAAMLALHVALWFLDAAHPILAVANFLGLTWLSVGL 60
 |||||
 DB 1 MSAAHLPRKADLTATSLIVSGGIIAAMLALHVALWFLDAAHPILAVANFLGLTWLSVGL 60

QY 61 FIITADHMGSVVPGPRANAMGOLVLMVYAGFSWRKKIVKMAHHRAGTDDDDPFH 120
 |||||
 DB 61 FIITADHMGSVVPGPRANAMGOLVLMVYAGFSWRKKIVKMAHHRAGTDDDDPFH 120

QY 121 GGPVRWYARFICTYFGMRGELLPIVITYYALMLGDRMWYVFWPLPSIIASIQLFVFGI 180
 |||||
 DB 121 GGPVRWYARFICTYFGMRGELLPIVITYYALMLGDRMWYVFWPLPSIIASIQLFVFGI 180

QY 181 WLPHRPGHDAPDRRNAASSRISDPVSLTCTHFGGYHHEHHLHPTVPMWRLPSTRTKGD 240
 |||||
 DB 181 WLPHRPGHDAPDRRNAASSRISDPVSLTCTHFGGYHHEHHLHPTVPMWRLPSTRTKGD 240

QY 241 TA 242
 |||||
 DB 241 TA 242

RESULT 3
 ADO61161
 ID ADO61161 standard; protein; 242 AA.

AC ADO61161;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE P. marcusii ketolase.
 XX
 KM ketocarotenoid; plant; ketolase; petal; flower-specific promoter;
 KM beta-specific promoter; epsilon-cyclase; ec; chromoplast; hydroxylase;
 KM beta-cyclase; bc; astaxanthin; canthaxanthin; echinenone; adonitubin;
 KM adonixanthin; ornamental; food; animal feed; supplement; pigment;
 KM colouring; trout; salmon; shrimp; enzyme.
 XX
 OS Paracoccus marcusii.
 XX
 PN DE10238978-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 20-AUG-2002; 2002DE-01038978.
 XX
 PR 20-AUG-2002; 2002DE-01038978.
 XX
 PA (SUNG-) SUNGENE GMBH & CO KGAA.
 XX

DR WPI, 2004-215840/21.
 DR N-PSDB; ADO61160.
 PT Method for preparing ketocarotenoids, useful e.g. as food or feed
 PT supplements, by increasing, or introducing, ketolase activity in the
 PT fruits of transgenic plants, also new nucleic acid constructs.
 XX
 PS Disclosure; SEQ ID NO 10; 77pp; German.
 XX
 CC This invention describes a novel method for preparing ketocarotenoids by
 CC culturing genetically modified plants that, in comparison with the wild-
 CC type, have altered ketolase activity in the fruits. The invention also
 CC describes a nucleic acid construct comprising a fruit-specific promoter
 CC linked functionally to a sequence that encodes the altered ketolase,
 CC genetically modified plants in which the fruits have altered ketolase
 CC activity and method for preparing such plants. The plants contain at
 CC least one nucleic acid sequence that encodes the ketolase, especially
 CC under control of a fruit-specific promoter, and particularly they contain
 CC chromoplasts in the fruit. The ketolase-encoding nucleic acid is inserted
 CC by standard methods, then the transgenic plants are cultivated, harvested
 CC and ketocarotenoids are isolated from their fruits. Preferred carotenoids
 CC include, astaxanthin, canthaxanthin, echinenone (or its 3- or 3'-hydroxy
 CC derivatives) adonirubin or adonixanthin. The modified plants with
 CC increased ketolase activity are used as ornamentals as food or animal
 CC feed and for preparation of ketocarotenoids-containing extracts or for
 CC preparing food/feed supplements, e.g., especially where the
 CC ketocarotenoid is astaxanthin, as a pigment for colouring trout, salmon
 CC and shrimp. The transgenic plants produce fruits with increased content
 CC of ketocarotenoids. The invention describes a construct, vector pSKRTO2
 CC which comprises, in pSUN5, a cassette containing the constitutive double
 CC 35S cauliflower mosaic virus promoter; the rbcS chloroplast transit
 CC peptide; the ketolase gene from *Haemococcus pluvialis* and a terminator.
 CC It was used to transform tomato cells, using *Agrobacterium tumefaciens*,
 CC and the infected cells regenerated to plants conventionally. One of the
 CC resulting transgenic lines, CS13-24, produced fruits that contained
 CC lycopene, beta-carotene, canthaxanthin, adonirubin or astaxanthin, but
 CC the last three were absent from wild-type fruits (which additionally
 CC contained lutein, not detected in transgenic fruits).
 CC
 XX Sequence 242 AA;
 SQ
 Query Match 99.3%; Score 1332; DB 8; Length 242;
 Best Local Similarity 99.2%; Pred. No. 4.7e-142;
 Matches 240; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSAAHLPKADLTATSLIVSGGIIAAMLAHVALHFLDAAPILAVANFLGLTWLSVGL 60
 DB 1 MSAAHLPKADLTATSLIVSGGIIAAMLAHVALHFLDAAPILAVANFLGLTWLSVGL 60
 QY 61 FIIADHAMGCVVPGRRPRANAMGCVLWLYAGFSRKRKIVKMAHHRAGTDDDDPDDH 120
 DB 61 FIIADHAMGCVVPGRRPRANAMGCVLWLYAGFSRKRKIVKMAHHRAGTDDDDPDDH 120
 QY 121 GGPVRYARFICGTFCMRGGLLPVIVTVYALMLGRRMMYVFWPSPILASIQLVFPGI 180
 DB 121 GGPVRYARFICGTFCMRGGLLPVIVTVYALMLGRRMMYVFWPSPILASIQLVFPGI 180
 QY 181 WLPHRGHDAPDRNANASSRISDPVSLITCFHFGYVHHHHLHPTVPMWRLESTRTKGD 240
 DB 181 WLPHRGHDAPDRNANASSRISDPVSLITCFHFGYVHHHHLHPTVPMWRLESTRTKGD 240
 QY 241 TA 242
 DB 241 TA 242
 DT 15-JUL-2004 (first entry)

XX
 DB P. marcusii ketolase.
 XX
 KW ketocarotenoid; plant; ketolase; petal; flower-specific promoter;
 KW petal-specific promoter; epsilon-cyclase; ec; chromoplast; hydroxylase;
 KW beta-cyclase; bc; astaxanthin; canthaxanthin; echinenone; adonirubin;
 KW adonixanthin; ornamental; food; animal feed; supplement; pigment;
 KW colouring; trout; salmon; shrimp; enzyme.
 XX
 OS Paracoccus marcusii.
 XX
 PN DE10238980-A1.
 XX
 PD 04-MAR-2004.
 XX
 XX 20-AUG-2002; 2002DE-01038980.
 XX
 XX 20-AUG-2002; 2002DE-01038980.
 XX
 PA (SUNG-) SUNGENE GMBH & CO KGAA.
 XX
 DR WPI, 2004-215842/21.
 DR N-PSDB; ADO61077.
 PT Method for preparing ketocarotenoids, useful e.g. as food or feed
 PT supplements, by increasing, or introducing, ketolase activity in the
 PT petals of transgenic plants, also new nucleic acid constructs.
 XX
 PS Disclosure; SEQ ID NO 10; 140pp; German.
 XX
 CC This invention describes a novel method for preparing ketocarotenoids by
 CC culturing genetically modified plants that, in comparison with the wild-
 CC type, have altered ketolase activity in the petals. The invention also
 CC describes a nucleic acid construct containing a nucleic acid that encodes
 CC ketolase, linked functionally to a flower- or petal-specific promoter,
 CC double-stranded RNA that comprises a sense strand, including a sequence
 CC that is essentially identical with at least part of the RNA epsilon-
 CC cyclase (ec) transcript or the promoter region of the ec gene and an
 CC antisense strand that is essentially complementary to the sense strand,
 CC an transgenic expression cassette comprising a plant-functional promoter
 CC linked to a nucleic acid that transcribes double-stranded RNA.
 CC genetically altered plant in which activity of ketolase in the petals is
 CC increased, if already present in the wild-type or introduced if absent
 CC from the wild type, genetically altered plant that has chromoplasts in
 CC the petals and contains at least one transgenic nucleic acid that encodes
 CC a ketolase. Particularly plants also have increased activity, relative to
 CC wild type, of hydroxylase and/or beta-cyclase (bc) activity, especially
 CC as a result of introducing the appropriate nucleic acid, and plants are
 CC also selected for highest activity of these two enzymes. The transgenic
 CC plants are cultivated, harvested and ketocarotenoids isolated from their
 CC petals. Preferred carotenoids include astaxanthin, canthaxanthin,
 CC echinenone (or its 3- or 3'-hydroxy derivatives), adonirubin or
 CC adonixanthin. The modified plants with increased ketolase activity are
 CC used as ornamentals, as food or animal feed and for preparation of
 CC ketocarotenoid-containing extracts or for preparing food/feed
 CC supplements, e.g., especially where the ketocarotenoid is astaxanthin, as
 CC a pigment for colouring trout, salmon and shrimp. The transgenic plants
 CC have increased content of ketocarotenoids. Vector pSKRTO2 comprises, in
 CC pSUN5, a cassette containing the constitutive double 35S cauliflower
 CC mosaic virus promoter, the rbcS chloroplast transit peptide, the ketolase
 CC gene from *Haemococcus pluvialis* and a terminator. The vector was used to
 CC transform tomato cells, using *Agrobacterium tumefaciens* and the infected
 CC cells regenerated to plants conventionally. One of the resulting
 CC transgenic lines, CS13-8, produced orange flowers (yellow in the wild
 CC type) and its petals contained astaxanthin and adonixanthin, both absent
 CC from the wild type.
 XX
 SQ Sequence 242 AA;
 Query Match 99.3%; Score 1332; DB 8; Length 242;
 Best Local Similarity 99.2%; Pred. No. 4.7e-142;
 Matches 240; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 MSAHALPRADLTATSLIVSGGIIAAMLAHVHLMFLDAAHPILAANFLGLTWLSVGL 60
DB 1 MSAHALPRADLTATSLIVSGGIIAAMLAHVHLMFLDAAHPILAANFLGLTWLSVGL 60
OY 61 FIHADAMHGSVVPGRPRANAMGQLVLMVYAGFSMRKIVYKMAHHRHAGTDDDDPDFH 120
DB 61 FIHADAMHGSVVPGRPRANAMGQLVLMVYAGFSMRKIVYKMAHHRHAGTDDDDPDFH 120
OY 121 GGPVWYARFICTYFGWREGLLPVIVVYVALMLGDRMYYVFWPLPSILASIQFVFGI 180
DB 121 GGPVWYARFICTYFGWREGLLPVIVVYVALMLGDRMYYVFWPLPSILASIQFVFGI 180
OY 181 WLPHRPGHDAPPDRNANASSRISDPVSLTCTHFGGYHHEHHLHPTVPMWRLPSTRKGD 240
DB 181 WLPHRPGHDAPPDRNANASSRISDPVSLTCTHFGGYHHEHHLHPTVPMWRLPSTRKGD 240
OY 241 TA 242
DB 241 TA 242

RESULT 5
ADQ38247
ID ADQ38247 standard, protein, 242 AA.
XX
AC ADQ38247;
XX
DT 23-SEP-2004 (first entry)
XX
DE Paracoccus marcusii ketolase.
XX
KW astaxanthin; plant; animal feed; fodder; fish; crustacean; bird;
KW salmonid; shrimp; crab; hen; duck; geese; flamingo; ketolase;
KW beta-carotene; canthaxanthin; hydroxylase; beta-cyclase; pigmentation;
KW trout; salmon; shrimp.
XX
OS Paracoccus marcusii.
XX
PN DE10258971-A1.
XX
PD 01-JUL-2004.
XX
PF 16-DEC-2002; 2002DE-01058971.
XX
PR 16-DEC-2002; 2002DE-01058971.
XX
PA (SUNG-) SUNGENE GMBH & CO KGAA.
XX
DR WPI; 2004-554601/54.
DR N-PSDB; ADQ38246.
XX
PT Use of astaxanthin-containing plant material, or extracts, from Tagetes
PT for oral administration to animals, particularly for pigmentation of
PT fish, crustacea, birds and their products.
XX
PS Disclosure; SEQ ID NO 10; 145bp; German.
XX
XX This invention describes the novel use of astaxanthin-containing plants
XX (particularly the flower heads or petals) of the genus Tagetes or their
XX parts for oral administration to animals. Methods are also described for
XX a) the preparation of an animal feed composition by mixing standard
XX fodder ingredients with astaxanthin-containing plants, b) for
XX pigmentation of animals, or their products, by oral administration of
XX astaxanthin-containing plants and c) animal feed composition or
XX pigmentation agent that contains astaxanthin-containing plants. The
XX plants, or their parts or extracts, are administered directly to animals,
XX optionally after intermediate processing, or they are formulated with
XX fodder components. Particularly they are administered to fish,
XX crustaceans or birds, specifically salmonids, shrimps, crabs, hens,
XX ducks, geese and flamingoes. The plants of the invention are preferably
XX modified to provide ketolase activity, for conversion of beta-carotene to
XX canthaxanthin, particularly with the highest level of expression in the
XX flowers, e.g. by using a flower-specific promoter. The plants may also

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CC have increased activity of hydroxylase (for conversion of canthaxanthin to astaxanthin) and/or of beta-cyclase (to increase production of beta-carotene from gamma-carotene). Astaxanthin-containing compositions are used particularly for pigmentation of animals, preferably fish, crustacea and birds, or their products (meat, skin, feathers and eggs), most particularly trout, salmon and shrimp. Genetically modified Tagetes produce larger amounts of astaxanthin than the current source, Adonis aestivialis, and more cheaply. The invention uses expression vector pSKETO2 which includes a cassette consisting of the double 35S promoter, the sequence for the pea rbc transit peptide, the sequence encoding a ketolase (beta-carotene-4-oxygenase) from Haematococcus pluvialis and the polyadenylation signal from cauliflower mosaic virus. It was used to transform leaves of Tagetes, by Agrobacterium-mediated transfer, then these regenerated to plants.

Sequence 242 AA;

Query Match 99.3%; Score 1332; DB 8; Length 242;
Best Local Similarity 99.2%; Pred. No. 4,7e-142;
Matches 240; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MSAHALPRADLTATSLIVSGGIIAAMLAHVHLMFLDAAHPILAANFLGLTWLSVGL 60
DB 1 MSAHALPRADLTATSLIVSGGIIAAMLAHVHLMFLDAAHPILAANFLGLTWLSVGL 60
OY 61 FIHADAMHGSVVPGRPRANAMGQLVLMVYAGFSMRKIVYKMAHHRHAGTDDDDPDFH 120
DB 61 FIHADAMHGSVVPGRPRANAMGQLVLMVYAGFSMRKIVYKMAHHRHAGTDDDDPDFH 120
OY 121 GGPVWYARFICTYFGWREGLLPVIVVYVALMLGDRMYYVFWPLPSILASIQFVFGI 180
DB 121 GGPVWYARFICTYFGWREGLLPVIVVYVALMLGDRMYYVFWPLPSILASIQFVFGI 180
OY 181 WLPHRPGHDAPPDRNANASSRISDPVSLTCTHFGGYHHEHHLHPTVPMWRLPSTRKGD 240
DB 181 WLPHRPGHDAPPDRNANASSRISDPVSLTCTHFGGYHHEHHLHPTVPMWRLPSTRKGD 240
OY 241 TA 242
DB 241 TA 242

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RESULT 6
ADRO3862
ID ADRO3862 standard, protein, 242 AA.
XX
AC ADRO3862;
XX
DT 21-OCT-2004 (first entry)
XX
DE Paracoccus marcusii ketolase SEQ ID NO: 20.
XX
KW carotenoid; genetically modified; Blakeslea; nutrient; pigmentation;
KW antioxidant; transgenic; ketolase; enzyme.
XX
XX Paracoccus marcusii.
XX
OS Synthetic.
XX
PN WO2004063359-A2.
XX
PD 29-JUL-2004.
XX
PF 09-JAN-2004; 2004WO-EP000099.
XX
PR 09-JAN-2003; 2003DE-01000649.
XX
PR 08-SEP-2003; 2003DE-01041271.
XX
PA (BADI ) BASF AG.
XX
PI Matschek M, Klein D, Heinekamp T, Schmidt A, Brakhage A;
XX Achatz B;
XX WPI; 2004-544088/52.
DR

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DR N-PSDB; ADR03861.

XX Preparing carotenoids or their precursors useful e.g. in cosmetics,
PT pharmaceuticals, foods and animal feeds, comprises culturing genetically
XX modified *Blakeslea*.

PS Disclosure; SEQ ID NO 20; 486bp; German.

CC The present invention relates to a method of preparing carotenoids or
CC their precursors using genetically modified organisms of the genus
CC *Blakeslea*. The method is used for production of carotenoids, particularly
CC carotenes and xanthophylls, useful as animal and human nutrients, or
CC supplements, cosmetics, dermatological agents and pharmaceuticals,
CC particularly for pigmentation or colouring beverages, but also as
CC antioxidants. The present sequence is a protein used in the
CC exemplification of the invention.

XX Sequence 242 AA;

Query Match 99.3%; Score 1332; DB 8; Length 242;
Best Local Similarity 99.2%; Pred. No. 4.7e-142;
Matches 240; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSAAALPKADLTATSLIVSGGIIAAMLAHVHAWFLDAAAHPIIAVANFLGLTWLSVGL 60
DB 1 MSAAALPKADLTATSLIVSGGIIAAMLAHVHAWFLDAAAHPIIAVANFLGLTWLSVGL 60
QY 61 FIIAHDAMGVSVPGRPRANAMGOLVLTLYAGFSWRKMIYKMAHHRHAGTDDDPDFH 120
DB 61 FIIAHDAMGVSVPGRPRANAMGOLVLTLYAGFSWRKMIYKMAHHRHAGTDDDPDFH 120
QY 121 GGPVRYARFITYGMRBGLLPVIVVYALMLGDRMYVVFVWPLPSIIASIQLFVFGI 180
DB 121 GGPVRYARFITYGMRBGLLPVIVVYALMLGDRMYVVFVWPLPSIIASIQLFVFGI 180
QY 181 WLPHRPGHDAFPDRHNAASRSISDPVSLITCFHFGYHHEHHLAPTVPMWRLPSTRTKGD 240
DB 181 WLPHRPGHDAFPDRHNAASRSISDPVSLITCFHFGYHHEHHLAPTVPMWRLPSTRTKGD 240
QY 241 TA 242
DB 241 TA 242

RESULT 7

ADR03942
ID ADR03942 standard; protein; 242 AA.

AC ADR03942;

DT 21-OCT-2004 (first entry)

DE P marcusii ketolase.

KW genetically modified; vector; carotenoid production; pigmentation;
KM nutrient; antioxidant; ketolase; enzyme.

OS Paracoccus marcusii.
OS Synthetic.

PN WO2004063358-A1.

PD 29-JUL-2004.

PF 09-JAN-2004; 2004WO-EP000100.

PR 09-JAN-2003; 2003DE-01000649.
PR 08-SEP-2003; 2003DE-01041272.

PA (BADT) BASF AG.

PI Matuschek M, Heinekamp T, Schmidt A, Brakhage A;

XX

DR MPI; 2004-544087/52.

DR N-PSDB; ADR03941.

XX Preparing genetically modified *Blakeslea*, useful for preparation of
PT carotenoids, useful as food additives, cosmetics or pharmaceuticals,
XX comprises transformation, optional homokaryotizing, and selection.

PS Disclosure; SEQ ID NO 20; 459bp; German.

CC The present invention relates to a method of preparing a genetically
CC modified organism of the genus *Blakeslea*, which comprises first
CC transforming at least one cell then optionally homokaryotizing the cells
CC so that cells are produced in which the nuclei are all simultaneously
CC altered in one or more genetic characteristics and these alterations are
CC expressed, and finally selection and culture of the modified cell(s). The
CC genetically modified organisms are used for the production of
CC carotenoids, particularly carotenes and xanthophylls, useful as animal
CC and human nutrients, or supplements, cosmetics and pharmaceuticals,
CC particularly for pigmentation or colouring beverages, but also as
CC antioxidants. The present sequence is a protein shown in the
CC exemplification of the invention.

XX Sequence 242 AA;

Query Match 99.3%; Score 1332; DB 8; Length 242;
Best Local Similarity 99.2%; Pred. No. 4.7e-142;
Matches 240; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSAAALPKADLTATSLIVSGGIIAAMLAHVHAWFLDAAAHPIIAVANFLGLTWLSVGL 60
DB 1 MSAAALPKADLTATSLIVSGGIIAAMLAHVHAWFLDAAAHPIIAVANFLGLTWLSVGL 60
QY 61 FIIAHDAMGVSVPGRPRANAMGOLVLTLYAGFSWRKMIYKMAHHRHAGTDDDPDFH 120
DB 61 FIIAHDAMGVSVPGRPRANAMGOLVLTLYAGFSWRKMIYKMAHHRHAGTDDDPDFH 120
QY 121 GGPVRYARFITYGMRBGLLPVIVVYALMLGDRMYVVFVWPLPSIIASIQLFVFGI 180
DB 121 GGPVRYARFITYGMRBGLLPVIVVYALMLGDRMYVVFVWPLPSIIASIQLFVFGI 180
QY 181 WLPHRPGHDAFPDRHNAASRSISDPVSLITCFHFGYHHEHHLAPTVPMWRLPSTRTKGD 240
DB 181 WLPHRPGHDAFPDRHNAASRSISDPVSLITCFHFGYHHEHHLAPTVPMWRLPSTRTKGD 240
QY 241 TA 242
DB 241 TA 242

RESULT 8

ADQ96834
ID ADQ96834 standard; protein; 648 AA.

AC ADQ96834;

DT 23-SEP-2004 (first entry)

DE CrtWcrty amino acid sequence.

KW carotenoid; transgenic plant; overlapping extension PCR amplification;
KM PCR; crtB; crtI; crtW; crtZ; astaxanthin; carotene;
KM grain crop; vegetable; crtWcrty.

OS Unidentified.

PN CN1380415-A.

PD 20-NOV-2002.

PF 06-APR-2001; 2001CN-00105878.

PR 06-APR-2001; 2001CN-00105878.

XX

PA (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.
XX
XX Yao Q, Peng R, Xiong A;
PI
XX WPI: 2003-230997/23.
DR N-PSDB; ADQ96833, ADQ96933.
XX
PT Synthesis of related gene for producing carotenoid in transgenic plant,
PT useful for improving quality of grain crops and vegetable.
XX
PS Claim 2; Page 1-2; 36pp; Chinese.
XX
CC The present invention relates to a related gene for producing carotenoid
CC in transgenic plant. The invention utilizes an overlapping extension PCR
CC amplification process and uses six genes of crtB, crtY, crtI, crtW, crtY
CC and crtZ as templates to synthesise the related gene for synthesising
CC astaxanthin with plant preference code and can make a synthetic gene for
CC expression in a plant to produce the carotene substances of astaxanthin.
CC The synthetic gene can be used to improve the quality of grain crops and
CC vegetables. The present sequence represents a specifically claimed
CC crtWcrtY amino acid sequence, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 648 AA;

Query Match 99.3%; Score 1332; DB 7; Length 648;
Best Local Similarity 99.2%; Pred. No. 1.7e-141;
Matches 240; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSAHALPKADLTATSLIVSGGIIAAMLAHVHAFDAAHPITLAVANFLGLTWLSVGL 60
DB 1 MSAHALPKADLTATSLIVSGGIIAAMLAHVHAFDAAHPITLAVANFLGLTWLSVGL 60
QY 61 FIHADAHGVSVPGRPRANAMGOLVLMVAGFSWRKMTVGMHHRHAGTDDDDPDH 120
DB 61 FIHADAHGVSVPGRPRANAMGOLVLMVAGFSWRKMTVGMHHRHAGTDDDDPDH 120
QY 121 GGPVWYARFIGTGYGMRGELLPIVTVVYALMLGDRMYYVFWPLPSILASIQLFVFGI 180
DB 121 GGPVWYARFIGTGYGMRGELLPIVTVVYALMLGDRMYYVFWPLPSILASIQLFVFGI 180
QY 181 WLPHRPGHDAPPDRHNARSSRISDPVSLTCTFHFSGYHHEHHLPTVPMWRLPSTRYKGD 240
DB 181 WLPHRPGHDAPPDRHNARSSRISDPVSLTCTFHFSGYHHEHHLPTVPMWRLPSTRYKGD 240
QY 241 TA 242
DB 241 TA 242

RESULT 9
AAW82260
ID AAW82260 standard; protein; 242 AA.
XX
XX AAW82260;

AC 17-OCT-2003 (revised)
DT 16-JUL-1999 (first entry)
XX
XX C. utilis crtW protein.
XX
XX HMG-CoA; 3-hydroxy-3-methylglutaryl coenzyme A reductase; crtW;
KW carotenoid.
XX
XX Pichia jadinii.
XX
XX JP10248575-A.
XX
XX 22-SEP-1998.
XX
XX 12-MAR-1997; 97JP-00058012.
XX
XX 12-MAR-1997; 97JP-00058012.
XX
XX

XX (KIRI) KIRIN BREWERY KK.
PA
XX
XX WPI: 1998-560727/48.
DR N-PSDB; AAV73184.
XX
PT Gene useful for increase in carotenoid production - and preparation of
PT carotenoid.
XX
PS Example 2; Fig 20-21; 54pp; Japanese.
XX
CC This invention describes a novel method for the preparation of
CC carotenoids using genes and proteins isolated from Candida utilis. The
CC invention specifically describes the isolation of a 3-hydroxy-3-
CC methylglutaryl coenzyme A (HMG-CoA) reductase protein. This sequence
CC represents the Candida utilis crtW protein which is used in the method of
CC the invention. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 242 AA;

Query Match 99.3%; Score 1331; DB 2; Length 242;
Best Local Similarity 98.8%; Pred. No. 6e-142;
Matches 239; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSAHALPKADLTATSLIVSGGIIAAMLAHVHAFDAAHPITLAVANFLGLTWLSVGL 60
DB 1 MSAHALPKADLTATSLIVSGGIIAAMLAHVHAFDAAHPITLAVANFLGLTWLSVGL 60
QY 61 FIHADAHGVSVPGRPRANAMGOLVLMVAGFSWRKMTVGMHHRHAGTDDDDPDH 120
DB 61 FIHADAHGVSVPGRPRANAMGOLVLMVAGFSWRKMTVGMHHRHAGTDDDDPDH 120
QY 121 GGPVWYARFIGTGYGMRGELLPIVTVVYALMLGDRMYYVFWPLPSILASIQLFVFGI 180
DB 121 GGPVWYARFIGTGYGMRGELLPIVTVVYALMLGDRMYYVFWPLPSILASIQLFVFGI 180
QY 181 WLPHRPGHDAPPDRHNARSSRISDPVSLTCTFHFSGYHHEHHLPTVPMWRLPSTRYKGD 240
DB 181 WLPHRPGHDAPPDRHNARSSRISDPVSLTCTFHFSGYHHEHHLPTVPMWRLPSTRYKGD 240
QY 241 TA 242
DB 241 TA 242

RESULT 10
ADO61157
ID ADO61157 standard; protein; 242 AA.
XX
XX ADO61157;

DT 15-JUL-2004 (first entry)
XX
XX A. aurantiacum ketolase.
DE

KW ketocarotenoid; plant; ketolase; petal; flower-specific promoter;
KW petal-specific promoter; epsilon-cyclase; ec; chromoplas; hydroxylase;
KW beta-cyclase; bc; astaxanthin; canthaxanthin; echinone; adonirubin;
KW adonixanthin; ornamental; food; animal feed; supplement; pigment;
KW colouring; trout; salmon; shrimp; enzyme.
XX

OS Agrobacterium aurantiacum.
XX

PN DE10238978-A1.
XX

PD 04-MAR-2004.
XX

PF 20-AUG-2002; 2002DE-01038978.
XX

PR 20-AUG-2002; 2002DE-01038978.
XX

PA (SUNG-) SUNGENE GMBH & CO KGAA.
XX

DR WPI; 2004-215840/21.
 XX N-PSDB; ADO61156.
 PT Method for preparing ketocarotenoids, useful e.g. as food or feed
 PT supplements, by increasing, or introducing, ketolase activity in the
 PT fruits of transgenic plants, also new nucleic acid constructs.
 XX
 PS Disclosure; SEQ ID NO 6; 77bp; German.
 XX
 CC This invention describes a novel method for preparing ketocarotenoid by
 CC culturing genetically modified plants that, in comparison with the wild-
 CC type, have altered ketolase activity in the fruits. The invention also
 CC describes a nucleic acid construct comprising a fruit-specific promoter
 CC linked functionally to a sequence that encodes the altered ketolase,
 CC genetically modified plants in which the fruits have altered ketolase
 CC activity and method for preparing such plants. The plants contain at
 CC least one nucleic acid sequence that encodes the ketolase, especially
 CC under control of a fruit-specific promoter, and particularly they contain
 CC chromoplasts in the fruit. The ketolase-encoding nucleic acid is inserted
 CC by standard methods, then the transgenic plants are cultivated, harvested
 CC and ketocarotenoids are isolated from their fruits. Preferred carotenoids
 CC include astaxanthin, canthaxanthin, echinenone (or its 3- or 3'-hydroxy
 CC derivatives) adonirubin or adonixanthin. The modified plants with
 CC increased ketolase activity are used as ornamentals as food or animal
 CC feed and for preparation of ketocarotenoids-containing extracts or for
 CC preparing food/feed supplements, e.g., especially where the
 CC ketocarotenoid is astaxanthin, as a pigment for colouring trout, salmon
 CC and shrimps. The transgenic plants produce fruits with increased content
 CC of ketocarotenoids. The invention describes a construct, vector p53KET02
 CC which comprises, in pSUN5, a cassette containing the constitutive double
 CC 35S cauliflower mosaic virus promoter; the rbcS chloroplast transit
 CC peptide; the ketolase gene from *Haemococcus pluvialis* and a terminator.
 CC It was used to transform tomato cells, using *Agrobacterium tumefaciens*,
 CC and the infected cells regenerated to plants conventionally. One of the
 CC resulting transgenic lines, CS13-24, produced fruits that contained
 CC lycopene, beta-carotene, canthaxanthin, adonirubin or astaxanthin, but
 CC the last three were absent from wild-type fruits (which additionally
 CC contained lutein, not detected in transgenic fruits).
 CC
 XX
 SO Sequence 242 AA;
 Query Match 99.3%; Score 1331; DB 8; Length 242;
 Best Local Similarity 98.8%; Pred. No. 6e-142;
 Matches 239; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSAAALPKADLTSLVSGGIIAAMTALVHALVFLDAAPITLAVANLTGLTWSVGL 60
 DB 1 MSAAALPKADLTSLVSGGIIAAMTALVHALVFLDAAPITLAVANLTGLTWSVGL 60
 QY 61 FIIAHDMGSGVVPGRPRANAAGOLVLMYAGFSRKMIVKMAHHRHAGTDDDDPDH 120
 DB 61 FIIAHDMGSGVVPGRPRANAAGOLVLMYAGFSRKMIVKMAHHRHAGTDDDDPDH 120
 QY 121 GGFVWYARITGYTFGRBGLLPVITYVALMGDRMWTVPWPLPSILASIOLEFVGI 180
 DB 121 GGFVWYARITGYTFGRBGLLPVITYVALMGDRMWTVPWPLPSILASIOLEFVGI 180
 QY 181 WLFHRGCHDAFPPRRNARSRIIDPVSLTCTFFGFGYHNEHLHPVPMWRLPSTRTKD 240
 DB 181 WLFHRGCHDAFPPRRNARSRIIDPVSLTCTFFGFGYHNEHLHPVPMWRLPSTRTKD 240
 QY 241 TA 242
 DB 241 TA 242

RESULT 11

ADO61074
 ID ADO61074 standard; protein; 242 AA.
 XX ADO61074;
 AC
 XX 15-JUL-2004 (first entry)
 DT

XX
 DE A. aurantiacum ketolase.
 XX
 KW ketocarotenoid; plant; ketolase; petal; flower-specific promoter;
 KW petal-specific promoter; epsilon-cyclase; ec; chromoplast; hydroxylase;
 KW beta-cyclase; bc; astaxanthin; canthaxanthin; echinenone; adonirubin;
 KW adonixanthin; ornamental; food; animal feed; supplement; pigment;
 KW colouring; trout; salmon; shrimp; enzyme.
 XX
 OS *Agrobacterium aurantiacum*.
 XX
 PN DE10238960-A1.
 XX
 PD 04-MAR-2004.
 XX
 PF 20-AUG-2002; 2002DE-01038980.
 XX
 PR 20-AUG-2002; 2002DE-01038980.
 XX
 PA (SUNG-) SUNGENE GMEH & CO KGMA.
 XX
 DR WPI; 2004-215842/21.
 XX N-PSDB; ADO61073.
 PT Method for preparing ketocarotenoids, useful e.g. as food or feed
 PT supplements, by increasing, or introducing, ketolase activity in the
 PT petals of transgenic plants, also new nucleic acid constructs.
 XX
 PS Disclosure; SEQ ID NO 6; 140bp; German.
 XX
 CC This invention describes a novel method for preparing ketocarotenoids by
 CC culturing genetically modified plants that, in comparison with the wild-
 CC type, have altered ketolase activity in the petals. The invention also
 CC describes a nucleic acid construct containing a nucleic acid that encodes
 CC ketolase, linked functionally to a flower- or petal-specific promoter,
 CC double-stranded RNA that comprises a sense strand, including a sequence
 CC that is essentially identical with at least part of the RNA epsilon-
 CC cyclase (ec) transcript or the promoter region of the ec gene and an
 CC antisense strand that is essentially complementary to the sense strand,
 CC an transgenic expression cassette comprising a plant-functional promoter
 CC linked to a nucleic acid that transcribes double-stranded RNA,
 CC genetically altered plant in which activity of ketolase in the petals is
 CC increased, if already present in the wild-type or introduced if absent
 CC from the wild type, genetically altered plant that has chromoplasts in
 CC the petals and contains at least one transgenic nucleic acid that encodes
 CC a ketolase. Particularly plants also have increased activity, relative to
 CC wild type, of hydroxylase and/or beta-cyclase (bc) activity, especially
 CC as a result of introducing the appropriate nucleic acid, and plants are
 CC also selected for highest activity of these two enzymes. The transgenic
 CC plants are cultivated, harvested and ketocarotenoids isolated from their
 CC petals. Preferred carotenoids include astaxanthin, canthaxanthin,
 CC echinenone (or its 3- or 3'-hydroxy derivatives), adonirubin or
 CC adonixanthin. The modified plants with increased ketolase activity are
 CC used as ornamentals, as food or animal feed and for preparation of
 CC ketocarotenoids-containing extracts or for preparing food/feed
 CC supplements, e.g., especially where the ketocarotenoid is astaxanthin, as
 CC a pigment for colouring trout, salmon and shrimps. The transgenic plants
 CC have increased content of ketocarotenoids. Vector p53KET02 comprises, in
 CC pSUN5, a cassette containing the constitutive double 35S cauliflower
 CC mosaic virus promoter, the rbcS chloroplast transit peptide, the ketolase
 CC gene from *Haemococcus pluvialis* and a terminator. The vector was used to
 CC transform tomato cells, using *Agrobacterium tumefaciens* and the infected
 CC cells regenerated to plants conventionally. One of the resulting
 CC transgenic lines, CS13-8, produced orange flowers (yellow in the wild
 CC type) and its petals contained astaxanthin and adonixanthin, both absent
 CC from the wild type.
 CC
 XX
 SO Sequence 242 AA;
 Query Match 99.3%; Score 1331; DB 8; Length 242;
 Best Local Similarity 98.8%; Pred. No. 6e-142;
 Matches 239; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DR N-PSDB; ADR03857.
 XX
 PT Preparing carotenoids or their precursors useful e.g. in cosmetics,
 PT pharmaceuticals, foods and animal feeds, comprises culturing genetically
 XX modified *Blakeslea*.
 XX
 PS Disclosure; SEQ ID NO 16; 486bp; German.
 CC
 CC The present invention relates to a method of preparing carotenoids or
 CC their precursors using genetically modified organisms of the genus
 CC *Blakeslea*. The method is used for production of carotenoids, particularly
 CC carotenes and xanthophylls, useful as animal and human nutrients, or
 CC supplements, cosmetics, dermatological agents and pharmaceuticals,
 CC particularly for pigmentation or colouring beverages, but also as
 CC antioxidants. The present sequence is a protein used in the
 CC exemplification of the invention.

CC
 CC Sequence 242 AA;

Query Match 99.3%; Score 1331; DB 8; Length 242;
 Best Local Similarity 98.8%; Pred. No. 6e-142;
 Matches 239; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNHALPKADLTATSLIVSGGIIAAMLAHVHLMFLDAAAHPIIAVANFLGLTWLSVGL 60
 DB 1 MSNHALPKADLTATSLIVSGGIIAAMLAHVHLMFLDAAAHPIIAVANFLGLTWLSVGL 60
 QY 61 FIIAHDAMGVSVPGRPRANAAMGOLVLMYAGFSRKMIVKMAHHRHAGTDDDDPDH 120
 DB 61 FIIAHDAMGVSVPGRPRANAAMGOLVLMYAGFSRKMIVKMAHHRHAGTDDDDPDH 120
 QY 121 GGPVRYARFIPTGYFGMRGGLLPVIVTVYALMLGDRMWVVFVFWPLPSIIASIQLFVFGI 180
 DB 121 GGPVRYARFIPTGYFGMRGGLLPVIVTVYALMLGDRMWVVFVFWPLPSIIASIQLFVFGI 180
 QY 181 WLPHRGHDAPDRNNAARSSRISDPVSLTCTFHFGYHHEHHLAPTVPMWRLLPSTRTKGD 240
 DB 181 WLPHRGHDAPDRNNAARSSRISDPVSLTCTFHFGYHHEHHLAPTVPMWRLLPSTRTKGD 240
 QY 241 TA 242
 DB 241 TA 242

RESULT 14
 ADR03938
 ID ADR03938 standard; protein; 242 AA.
 XX
 AC ADR03938;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE A aurantiacum ketolase.
 XX
 KM genetically modified; vector; carotenoid production; pigmentation;
 KM nutrient; antioxidant; ketolase; enzyme.
 XX
 OS *Agrobacterium aurantiacum*.
 OS Synthetic.
 XX
 PN WO2004063358-A1.
 XX
 PD 29-JUL-2004.
 XX
 PF 09-JAN-2004; 2004WO-EP000100.
 XX
 PR 09-JAN-2003; 2003DE-01000649-
 PR 08-SEP-2003; 2003DE-01041272.
 XX
 PA (BADI) BASF AG.
 XX
 PI Matuschek M, Heinkekamp T, Schmidt A, Brakhage A;
 XX

DR WPI; 2004-544087/52.
 DR N-PSDB; ADR03937.
 XX
 PT Preparing genetically modified *Blakeslea*, useful for preparation of
 PT carotenoids, useful as food additives, cosmetics or pharmaceuticals,
 PT comprises transformation, optional homokaryotizing, and selection.
 XX
 PS Disclosure; SEQ ID NO 16; 459bp; German.

CC The present invention relates to a method of preparing a genetically
 CC modified organism of the genus *Blakeslea*, which comprises first
 CC transforming at least one cell then optionally homokaryotizing the cells
 CC so that cells are produced in which the nuclei are all simultaneously
 CC altered in one or more genetic characteristics and these alterations are
 CC expressed, and finally selection and culture of the modified cell(s). The
 CC genetically modified organisms are used for the production of
 CC carotenoids, particularly carotenes and xanthophylls, useful as animal
 CC and human nutrients, or supplements, cosmetics and pharmaceuticals,
 CC particularly for pigmentation or colouring beverages, but also as
 CC antioxidants. The present sequence is a protein shown in the
 CC exemplification of the invention.

CC
 CC Sequence 242 AA;

Query Match 99.3%; Score 1331; DB 8; Length 242;
 Best Local Similarity 98.8%; Pred. No. 6e-142;
 Matches 239; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNHALPKADLTATSLIVSGGIIAAMLAHVHLMFLDAAAHPIIAVANFLGLTWLSVGL 60
 DB 1 MSNHALPKADLTATSLIVSGGIIAAMLAHVHLMFLDAAAHPIIAVANFLGLTWLSVGL 60
 QY 61 FIIAHDAMGVSVPGRPRANAAMGOLVLMYAGFSRKMIVKMAHHRHAGTDDDDPDH 120
 DB 61 FIIAHDAMGVSVPGRPRANAAMGOLVLMYAGFSRKMIVKMAHHRHAGTDDDDPDH 120
 QY 121 GGPVRYARFIPTGYFGMRGGLLPVIVTVYALMLGDRMWVVFVFWPLPSIIASIQLFVFGI 180
 DB 121 GGPVRYARFIPTGYFGMRGGLLPVIVTVYALMLGDRMWVVFVFWPLPSIIASIQLFVFGI 180
 QY 181 WLPHRGHDAPDRNNAARSSRISDPVSLTCTFHFGYHHEHHLAPTVPMWRLLPSTRTKGD 240
 DB 181 WLPHRGHDAPDRNNAARSSRISDPVSLTCTFHFGYHHEHHLAPTVPMWRLLPSTRTKGD 240
 QY 241 TA 242
 DB 241 TA 242

RESULT 15
 AAW98198
 ID AAW98198 standard; protein; 299 AA.
 XX
 AC AAW98198;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE SSU/beta-carotene ketolase fusion.
 XX
 KM Btea-carotene ketolase; crtW gene; carotenoid; xanthophyll; pigment;
 KM astaxanthin; zeaxanthin; alpha-carotene; beta-carotene; phytoene;
 KM echinenone; canthaxanthin; transgenic plant; oilseed plant; seed oil;
 KM A. aurantiacum.
 XX
 OS unidentified.
 OS
 PN WO9907867-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 06-AUG-1998; 98WO-US016466.
 XX
 PR 08-AUG-1997; 97US-00908758.

```

XX (CALJ ) CALGENE LLC.
PA
XX Shewmaker CK;
PI
XX WPI, 1999-180495/15.
DR N-PSDB; AAX25068.
XX
PT Altering xanthophyll content of seeds by transformation - used to produce
XX seed oils of increased carotenoid content, e.g. Brassica and cotton.
XX
PS Example 1; Fig 16; 92pp; English.
XX
XX The present sequence is a fusion between a SSU leader and a beta-carotene
CC ketolase encoded by the crtW gene (see AAX25068) of A. aurantiacum. The
CC xanthophyll content of seeds can be altered by transforming cells of a
CC host plant with at least one construct containing: (i) a transcription
CC initiation region of a gene that is preferentially expressed in seeds;
CC (ii) the sequence for a plastid transit peptide; (iii) DNA from a
CC carotenoid synthesis gene coding region, and (iv) a transcription
CC terminator. The transformed cells are regenerated to plants and these, or
CC their progeny, grown to produce seeds. The method is especially used to
CC increase the carotenoid content in oilseed plants. Coexpression of beta-
CC carotene hydroxylase (see AA98197) and beta-carotene ketolase results in
CC increased astaxanthin and zeaxanthin content in the seeds of transformed
CC plants. Coexpression of beta-carotene ketolase with phytylase synthase
CC (see AAX25063) results in increased levels of alpha-carotene, beta-
CC carotene and phytylene, as well as echinenone and canthaxanthin
XX
SQ Sequence 299 AA;

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Query Match          98.9%; Score 1326; DB 2; Length 299;
Best Local Similarity 98.3%; Pred. No. 2.9e-141;
Matches 238; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSAAHLPKADLTATSLIVSGGIIAAMLAHVHAAFLDAAHPITLAVANFLGLTWLSVGL 60
   |||||
DB 58 MSAAHLPKADLTATSLIVSGGIIAAMLAHVHAAFLDAAHPITLAVANFLGLTWLSVGL 117

QY 61 FTIAHDAMHGSVYVPGRRANAAAGCOLVWLYAGFSRKMIVKMAHHRHAGTDDDPDFH 120
   |||||
DB 118 FTIAHDAMHGSVYVPGRRANAAAGCOLVWLYAGFSRKMIVKMAHHRHAGTDDDPDFH 177

QY 121 GGPVRWYARFIGTYFGMRBGLLPVIVTVYALMTGDRMYVVFVWPLPSILASIQLFVFGI 180
   |||||
DB 178 GGPVRWYARFIGTYFGMRBGLLPVIVTVYALMTGDRMYVVFVWPLPSILASIQLFVFGI 237

QY 181 WLPHRPGHDAPFDRNNAARSSRISDPVSLTCTHFGGTHHHHHLAPTVPMWRLLPSTRTKGD 240
   |||||
DB 238 WLPHRPGHDAPFDRNNAARSSRISDPVSLTCTHFGGTHHHHHLAPTVPMWRLLPSTRTKGD 297

QY 241 TA 242
   ||
DB 298 TA 299

```

Search completed: June 17, 2005, 19:33:05
 Job time : 90.1987 secs

GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsyanakov, Yuri
TITLE OF INVENTION: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)
CURRENT FILING DATE: 2001-08-02
PRIORITY FILING DATE: 1997-12-01
PRIORITY FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 32
LENGTH: 242
TYPE: PRP
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: E-396
US-09-920-923B-32

Query Match 100.0%; Score 1341; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 2,2e-140;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAHALPKADLTATSLIVSGGIIAAMLAHVHAFMDAAPIILAVANFLGLTWSGL 60
DB 1 MSAHALPKADLTATSLIVSGGIIAAMLAHVHAFMDAAPIILAVANFLGLTWSGL 60
QY 61 FLIAADAMGVSVPGRPRANAMGQVLMVYAGFSRKMIVKMAHHRAGTDDPDPDH 120
DB 61 FLIAADAMGVSVPGRPRANAMGQVLMVYAGFSRKMIVKMAHHRAGTDDPDPDH 120
QY 121 GSPVWYAFITGYFGMRGLLPVIVTYAALMDGRWYVFWPLPSILASIQLFVFGI 180
DB 121 GSPVWYAFITGYFGMRGLLPVIVTYAALMDGRWYVFWPLPSILASIQLFVFGI 180
QY 181 WLPHPGHDAFPDRNARSRI SDPVSLLTCHFGYHHEHLHPVPMWRIPSTRTKGD 240
DB 181 WLPHPGHDAFPDRNARSRI SDPVSLLTCHFGYHHEHLHPVPMWRIPSTRTKGD 240
QY 241 TA 242
DB 241 TA 242

RESULT 3

US-08-663-310-2
Sequence 2, Application US/08663310

GENERAL INFORMATION:
PATENT NO. 5811273
APPLICANT: MISAWA, No. 5811273hiko
APPLICANT: KONDO, Keiji
APPLICANT: KAJIWARA, Susumu
APPLICANT: YOKOYAMA, Akihito
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-663-310-2

Query Match 88.2%; Score 1183; DB 2; Length 212;
Best Local Similarity 98.6%; Pred. No. 5.8e-123;
Matches 209; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 31 VHALFLLDAAHPILAVANFLGLTWSGLFLIAADAMGVSVPGRPRANAMGQVLMV 90
DB 1 VHALFLLDAAHPILAVANFLGLTWSGLFLIAADAMGVSVPGRPRANAMGQVLMV 90
QY 91 YAGFSRKMIVKMAHHRAGTDDPDHGGPVWYAFITGYFGMRGLLPVIVTYV 150
DB 91 YAGFSRKMIVKMAHHRAGTDDPDHGGPVWYAFITGYFGMRGLLPVIVTYV 150
QY 151 ALMLGDRWYVFWPLPSILASIQLFVGIWLPHPGHDAFPDRNARSRI SDPVSLLT 210
DB 151 ALMLGDRWYVFWPLPSILASIQLFVGIWLPHPGHDAFPDRNARSRI SDPVSLLT 210
QY 211 CFHFGYHHEHLHPVPMWRIPSTRTKGDTA 242
DB 211 CFHFGYHHEHLHPVPMWRIPSTRTKGDTA 242

RESULT 4

US-09-006-491-2
Sequence 2, Application US/09006491

GENERAL INFORMATION:
PATENT NO. 5972690
APPLICANT: MISAWA, No. 5972690hiko
APPLICANT: KONDO, Keiji
APPLICANT: KAJIWARA, Susumu
APPLICANT: YOKOYAMA, Akihito
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,491

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-006-491-2

Query Match 88.2%; Score 1183; DB 2; Length 212;
Best Local Similarity 98.6%; Pred. No. 5,8e-123;
Matches 209; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 31 VHALWFLDAAHPILAVANFLGLTWLSVGLFTIADAMGSGVVPGRPRANAMGQLVLM 90
1 VHALWFLDAAHPILAVANFLGLTWLSVGLFTIADAMGSGVVPGRPRANAMGQLVLM 60
DB 91 YAGFSRKMIYVGMAMHRAHAGTDDPDHGGPVRWYAFIGTYFGMRGGLLPVIVTVY 150
61 YAGFSRKMIYVGMAMHRAHAGTDDPDHGGPVRWYAFIGTYFGMRGGLLPVIVTVY 120
QY 151 AALMDGRMYVFWPLPSILASIQLFVFGIWLPHRPGHDAFPDRNARSSRISDPVSLT 210
121 AALMDGRMYVFWPLPSILASIQLFVFGIWLPHRPGHDAFPDRNARSSRISDPVSLT 180
DB 211 CFHFGYHHEHHLPTVPMWRLPSTRTKGDTA 242
181 CFHFGYHHEHHLPTVPMWRLPSTRTKGDTA 212

RESULT 5
US-09-335-919-2
Sequence 2, Application US/09335919
Patent No. 6150130
GENERAL INFORMATION:
APPLICANT: MISAWA, No. 6150130ihko
APPLICANT: KONDO, Keiji
APPLICANT: KAJIWARA, Susumu
APPLICANT: YOKOYAMA, Akihito
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,919
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-335-919-2

Query Match 88.2%; Score 1183; DB 3; Length 212;
Best Local Similarity 98.6%; Pred. No. 5,8e-123;
Matches 209; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 31 VHALWFLDAAHPILAVANFLGLTWLSVGLFTIADAMGSGVVPGRPRANAMGQLVLM 90
1 VHALWFLDAAHPILAVANFLGLTWLSVGLFTIADAMGSGVVPGRPRANAMGQLVLM 60
DB 91 YAGFSRKMIYVGMAMHRAHAGTDDPDHGGPVRWYAFIGTYFGMRGGLLPVIVTVY 150
61 YAGFSRKMIYVGMAMHRAHAGTDDPDHGGPVRWYAFIGTYFGMRGGLLPVIVTVY 120
QY 151 AALMDGRMYVFWPLPSILASIQLFVFGIWLPHRPGHDAFPDRNARSSRISDPVSLT 210
121 AALMDGRMYVFWPLPSILASIQLFVFGIWLPHRPGHDAFPDRNARSSRISDPVSLT 180
DB 211 CFHFGYHHEHHLPTVPMWRLPSTRTKGDTA 242
181 CFHFGYHHEHHLPTVPMWRLPSTRTKGDTA 212

RESULT 6
US-08-663-310-9
Sequence 9, Application US/08663310
Patent No. 5811273
GENERAL INFORMATION:
APPLICANT: MISAWA, No. 5811273ihko
APPLICANT: KONDO, Keiji
APPLICANT: KAJIWARA, Susumu
APPLICANT: YOKOYAMA, Akihito
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA

```

; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,310
; FILING DATE: 23-SEP-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/02220
; FILING DATE: 26-DEC-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 6-235917
; FILING DATE: 05-SEP-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 5-348737
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 49441/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-663-310-9

```

```

Query Match      77.9%; Score 1044; DB 2; Length 242;
Best Local Similarity 77.5%; Pred. No. 1.7e-107;
Matches 179; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

```

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QY 12 TATSLIVSGGIIAAMALVHVALWFLDAAPHLAVANFLGLTWLSVGLFTIADAMGSG 71
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 12 TVVNLGLTALILCLVLAFTLMLDAAAPHLAVLCLAGLTWLSVGLFTIADAMGSG 71
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 72 VVPGPRPANAAGQLVLMYLAFSGFSWRKMIYKMAHHRHAGTDDEDFHGGFVRYARFI 131
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 72 VVPGPRPANAAGQLVLMYLAFSGFSWRKMIYKMAHHRHAGTDDEDFHGGFVRYARFI 131
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 132 GTFPGMRGGLLPVIVTVYALMLGDRMNVVFWPLPSIIASTIQLFVFGIWLPHRPGHDAF 191
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 132 STYFGMRGGLLPVIVTVYALMLGDRMNVVFWPVPVAVLASIQLFVFGIWLPHRPGHDAF 191
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 192 PDRHNARSGTIGDPLSLTLCFHFSGYHHEHHLHPVPMWRPLPRTKTKGDTA 242
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 192 PDRHNARSGTIGDPLSLTLCFHFSGYHHEHHLHPVPMWRPLPRTKTKGDTA 242
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 7
US-09-006-491-9
Sequence 9, Application US/09006491

```

; GENERAL INFORMATION:
; Patent No. 5972690
; APPLICANT: MISAHA, No. 5972690ihiko
; APPLICANT: KONDO, Keiji
; APPLICANT: KAJIWARA, Susumu
; APPLICANT: YOKOYAMA, Akihiro
; TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
; TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington

```

```

; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,491
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/663,310
; FILING DATE: 23-SEP-1996
; APPLICATION NUMBER: WO PCT/JP94/02220
; FILING DATE: 26-DEC-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 6-235917
; FILING DATE: 05-SEP-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 5-348737
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 49441/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-006-491-9

```

```

Query Match      77.9%; Score 1044; DB 2; Length 242;
Best Local Similarity 77.5%; Pred. No. 1.7e-107;
Matches 179; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

```

```

QY 12 TATSLIVSGGIIAAMALVHVALWFLDAAPHLAVANFLGLTWLSVGLFTIADAMGSG 71
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 12 TVVNLGLTALILCLVLAFTLMLDAAAPHLAVLCLAGLTWLSVGLFTIADAMGSG 71
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 72 VVPGPRPANAAGQLVLMYLAFSGFSWRKMIYKMAHHRHAGTDDEDFHGGFVRYARFI 131
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 72 VVPGPRPANAAGQLVLMYLAFSGFSWRKMIYKMAHHRHAGTDDEDFHGGFVRYARFI 131
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 132 GTFPGMRGGLLPVIVTVYALMLGDRMNVVFWPLPSIIASTIQLFVFGIWLPHRPGHDAF 191
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 132 STYFGMRGGLLPVIVTVYALMLGDRMNVVFWPVPVAVLASIQLFVFGIWLPHRPGHDAF 191
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 192 PDRHNARSGTIGDPLSLTLCFHFSGYHHEHHLHPVPMWRPLPRTKTKGDTA 242
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 192 PDRHNARSGTIGDPLSLTLCFHFSGYHHEHHLHPVPMWRPLPRTKTKGDTA 242
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

RESULT 8
US-09-335-919-9

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; Sequence 9, Application US/09335919
; Patent No. 6150130
; GENERAL INFORMATION:
; APPLICANT: MISAHA, No. 6150130ihiko
; APPLICANT: KONDO, Keiji
; APPLICANT: KAJIWARA, Susumu
; APPLICANT: YOKOYAMA, Akihiro
; TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
; TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
; NUMBER OF SEQUENCES: 12

```

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; CURRENT APPLICATION NUMBER: US/08/980,832B
; CURRENT FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Alcaligenes PC-1
US-08-980-832-29

Query Match      77.9%; Score 1044; DB 3; Length 242;
Best Local Similarity 77.5%; Pred. No. 1,7e-107;
Matches 179; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

QY      12  TATSLIVSGGIIAAMTALAHVHALMFDDAAHPILAVANFGLTWSGLFTIAHADAHGS 71
       12  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      12  TIVVLGLTAAILLCWLVIAFTLMLDRAAHPILAAVCLAGLTWSGLFTIAHADAHGS 71

QY      72  VVPRPPANAMAGOLVLMLYAGFSWRKMYIKSMAHHHHAAGTDDDPDGHGSPVAVARFI 131
       72  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      72  VVPRPPANAMAGOLALMLYAGFSWPKLIAKMTHTHHHAAGTDNDPDGHGSPVAVGSEFV 131

QY      132  GTYFGWREGLLPVTIVTVVYALMLGDRMMYVVFVPLPSILASIQLFVGIWLPHRPGDAF 191
       132  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      132  STYFGWREGLLPVTIVTVYALLIGDRMMYVIFVWPVAVLASIQIFVGIWLPHRPGHDDF 191

QY      192  PDRHNAASSRISDPVSLITCFHFHGGYHHEHHLHPTVWWRLLPSTRKTGDA 242
       192  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      192  PDRHNAASTGIGDPLSLITCFHFHGGYHHEHHLHPHVWWRLLPSTRKTGGA 242

RESULT 10
US-09-920-923B-29
; Sequence 29, Application US/09920923B
; Patent No. 6677134
; GENERAL INFORMATION:
; APPLICANT: Pasamontee, Luis
; TITLE OF INVENTION: Fermentative Carotenoid Production
; FILE REFERENCE: 15464 US (C38435/125944)
; CURRENT APPLICATION NUMBER: US/09/920,923B
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Alcaligenes PC-1
US-09-920-923B-29

Query Match      77.9%; Score 1044; DB 4; Length 242;
Best Local Similarity 77.5%; Pred. No. 1,7e-107;
Matches 179; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

QY      12  TATSLIVSGGIIAAMTALAHVHALMFDDAAHPILAVANFGLTWSGLFTIAHADAHGS 71
       12  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      12  TIVVLGLTAAILLCWLVIAFTLMLDRAAHPILAAVCLAGLTWSGLFTIAHADAHGS 71

QY      72  VVPRPPANAMAGOLVLMLYAGFSWRKMYIKSMAHHHHAAGTDDDPDGHGSPVAVARFI 131
       72  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      72  VVPRPPANAMAGOLALMLYAGFSWPKLIAKMTHTHHHAAGTDNDPDGHGSPVAVGSEFV 131

QY      132  GTYFGWREGLLPVTIVTVVYALMLGDRMMYVVFVPLPSILASIQLFVGIWLPHRPGDAF 191
       132  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      132  STYFGWREGLLPVTIVTVYALLIGDRMMYVIFVWPVAVLASIQIFVGIWLPHRPGHDDF 191

QY      192  PDRHNAASSRISDPVSLITCFHFHGGYHHEHHLHPTVWWRLLPSTRKTGDA 242
       192  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      192  PDRHNAASTGIGDPLSLITCFHFHGGYHHEHHLHPHVWWRLLPSTRKTGGA 242

```



```

1 GENERAL INFORMATION:
2 APPLICANT: Joseph Hirschberg, Tamar Lotan and
3 APPLICANT: Mark Harker
4 TITLE OF INVENTION: Polynucleotide molecule from
5 TITLE OF INVENTION: Haematococcus pluvialis encoding a
6 TITLE OF INVENTION: polypeptide having a beta-C-4-oxigenase
7 TITLE OF INVENTION: activity for biotechnological production of
8 TITLE OF INVENTION: (3S,3'S) astaxanthin.
9 NUMBER OF SEQUENCES: 4
10 CORRESPONDENCE ADDRESSES:
11 ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
12 STREET: 2001 Jefferson Davis Highway, Suite 207
13 CITY: Arlington
14 STATE: Virginia
15 COUNTRY: United States of America
16 ZIP: 22202
17
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
20 COMPUTER: Chicoma NB5500/386SX
21 OPERATING SYSTEM: MS DOS version 6.2,
22 SOFTWARE: word for Windows version 3.11
23 SOFTWARE: word for Windows version 2.0,
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/09/259,294
26 FILING DATE:
27
28 CLASSIFICATION:
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 08/742,605
31 FILING DATE: Oct. 28, 1996
32 APPLICATION NUMBER: 08/562,535
33 FILING DATE: No. 6218599, 24, 1995
34 ATTORNEY/AGENT INFORMATION:
35 NAME: Friedman, Mark M.
36 REGISTRATION NUMBER: 33, 883
37 REFERENCE/DOCKET NUMBER: 325/12
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: 972-3-562553
40 TELEFAX: 972-3-562554
41
42 TELEX:
43 INFORMATION FOR SEQ ID NO: 4:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 329 amino acids
46 TYPE: amino acid
47 TOPOLOGY: linear
48
49 US-09-259-294-4
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US-08-632-434-8
Sequence 8, Application US/06632434
Patent No. 5910433
GENERAL INFORMATION:
APPLICANT: KAJIWARA, Susumu
APPLICANT: MISAWA, No. 5910433jiko
APPLICANT: KONDO, Keiji
TITLE OF INVENTION: KETO GROUP-INTRODUCING ENZYME, DNA
TITLE OF INVENTION: CODING THEREFOR AND METHOD FOR PRODUCING KETOCAROTENOIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,434
FILING DATE: 23-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 95/047266
FILING DATE: 07-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 94/223798
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 94/198775
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 81356/106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-632-434-8

Query Match      25.5%; Score 342.5; DB 2; Length 288;
Best Local Similarity 31.7%; Pred. No. 1,1e-29;
Matches 84; Conservative 39; Mismatches 107; Indels 35; Gaps 8;

QY      3 AHALPKADLTATSLIVSGGIIAAVLALVHAL-----W-----FLDA 40
DB      16 AYKPPASDAKGIWTALT--IIGTAVFLHAIFOIRLPTSMNDQLHWLPVBATQQLGG 73
QY      41 AHLPLAVANPLGLTWISVGFLTIANDMHGSVVGRBRANAAMQGLVLMYAGSWMRKMI 100
DB      74 SSLHLIAVANFLVEFLTLTGFLTTHDMHGHTIALRHRLQDLNLGNITCSLYAFWDYSMLH 133
QY      101 VKHMAHRHAG-TDDDEPDFHGGP--VRWYARFIGTYFGWRKEGILLFVIIVTVVALMGDR 157
DB      134 RKHEHHNNHGEVKDDDFHKNGNGLVPWFSPFSSYMSLMQFARKLVANVAVMQMCLAMP 193
QY      158 WMYVFWPLPSIASIQLFVFGIWLPHRP-----GHDAFPDRHNNAASSRIIDPVSLITC 211
DB      194 ANLLVFMAAAPILISAPFLFYFGTYLPHKPEKGPAAGSQVMA-WFRATSEASDVMSFLTC 252
QY      212 FHFGYHNNHLLHPTVPMWRLPSTR 236

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Db 253 YHF-DLHWEHHRMPAPMWQLPHCR 276

RESULT 15

US-08-632-434-6
Sequence 6, Application US/08632434
Patent No. 5910433

GENERAL INFORMATION:

APPLICANT: KAJIMAWA, Susumu
APPLICANT: MISAWA, No. 5910433;hiko

APPLICANT: KONDO, Keiji

TITLE OF INVENTION: KETO GROUP-INTRODUCING ENZYME, DNA

TITLE OF INVENTION: CODING THEREFOR AND METHOD FOR PRODUCING KETOCAROTENOID

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/632,434

FILING DATE: 23-APR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 95/047266

FILING DATE: 07-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 94/223798

FILING DATE: 19-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 94/198775

FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 81356/106

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 313 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-632-434-6

Query Match 25.5%; Score 342.5; DB 2; Length 313;

Best Local Similarity 31.7%; Pred. No. 1.3e-29;

Matches 84; Conservative 39; Mismatches 107; Indels 35; Gaps 8;

QY 3 AHALPKADLTATSLIVSGGIAMALAHYAL-----W-----FLDAA 40

Db 41 AYKPPASDAKGIATMALT--IIGTWTAVFLHAIFQIRLPTSMQJHMLPVSEATAQLLGGS 98

QY 41 AHPILAVANFLGTLWLSVGLFIADAHGGSVVGPRANAAAGOLVWLVAAGFSWRKMI 100

Db 99 SSLIHIAAFVIVLEFLYTGIFITTHDAMGTTALRRQLNDLIGNICISLIAMFDYSMLH 158

QY 101 VKMAHRRHAG--TDDEPDPEHGGP--VRVYARFITYFGWRBGLPLVIVVYALMDGR 157

Db 159 RKGWEHNNHTGEGKDPDFHKNGPGLVPWFASFMSYMSLMQPARLAMWAVVMQMGAPM 218

QY 158 WMTVVVFWPLPSIIASIQLEVFEGIMLPHRP-----GHDAFPDRHNAARSSRIDPVSLLTC 211

Db 219 ANLVMAAAILSAFLFYFGTYLPHKPEEGPAAAGSOVMA-WFPAKTSASADVMSFLTC 277

QY 212 FAFGGYHEHHLLHPTVPMWRRLPSTR 236

Db 278 YHF-DLHWEHHRMPAPMWQLPHCR 301

Search completed: June 17, 2005, 19:39:11
Job time : 24.6571 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 17, 2005, 19:37:17 ; Search time 82.6058 Seconds
(without alignments)
1124.898 Million cell updates/sec

Title: US-10-695-980-32

Perfect score: 1341

Sequence: 1 MSAHALPKADLTATSLIVSG.....LHPTVPMRLPSTRKGDYA 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues 1714042

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA.*
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22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1341	100.0	242	10	US-09-920-923-32
2	1341	100.0	242	14	US-10-166-225A-181
3	1341	100.0	242	15	US-10-695-980-32
4	1341	99.3	242	18	US-10-997-844-33
5	1044	77.9	242	10	US-09-920-923-29
6	1044	77.9	242	15	US-10-695-980-29
7	564	42.1	244	15	US-10-466-656-39
8	564	42.1	244	17	US-10-848-307-39
9	354.5	26.4	329	9	US-09-791-687A-4
10	146	10.9	453	15	US-10-310-154-466
11	146	10.9	453	17	US-10-732-923-359

12	146	10.9	454	17	US-10-732-923-4850	Sequence 4850, Ap
13	145	10.8	363	17	US-10-732-923-4730	Sequence 4730, Ap
14	144	10.7	268	15	US-10-369-493-15558	Sequence 15558, A
15	144	10.7	280	15	US-10-369-493-15931	Sequence 15931, A
16	144	10.7	280	15	US-10-369-493-16296	Sequence 16296, A
17	144	10.7	298	17	US-10-200-545-90	Sequence 90, Appl
18	143.5	10.7	493	17	US-10-732-923-4742	Sequence 4742, Ap
19	141	10.5	447	16	US-10-425-115-310937	Sequence 310937, A
20	139.5	10.4	398	17	US-10-732-923-4809	Sequence 4809, Ap
21	139	10.4	341	14	US-10-314-657-20	Sequence 20, Appl
22	139	10.4	341	17	US-10-473-193-20	Sequence 20100, A
23	137	10.2	347	15	US-10-369-493-20100	Sequence 19077, A
24	135.5	10.1	350	15	US-10-369-493-19077	Sequence 28, Appl
25	135.5	10.1	366	14	US-10-115-571A-28	Sequence 4852, Ap
26	135.5	10.1	453	17	US-10-732-923-4852	Sequence 4853, Ap
27	135	10.1	424	17	US-10-732-923-4892	Sequence 4853, Ap
28	135	10.1	526	17	US-10-732-923-4853	Sequence 4795, Ap
29	134.5	10.0	385	17	US-10-732-923-4795	Sequence 19438, A
30	134	10.0	337	15	US-10-369-493-19438	Sequence 4891, Ap
31	134	10.0	349	17	US-10-732-923-4891	Sequence 310903, A
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33	134	10.0	443	16	US-10-425-115-310903	Sequence 4811, Ap
34	134	10.0	443	17	US-10-732-923-4810	Sequence 4807, Ap
35	134	10.0	433	17	US-10-732-923-4811	Sequence 4808, Ap
36	131.5	9.8	373	14	US-10-115-571A-27	Sequence 11971, A
37	131.5	9.8	398	17	US-10-732-923-4807	Sequence 4774, Ap
38	131.5	9.8	398	17	US-10-732-923-4808	Sequence 4816, Ap
39	130	9.7	340	15	US-10-369-493-11971	Sequence 33, Appl
40	130	9.7	340	17	US-10-732-923-4774	Sequence 4804, Ap
41	129	9.6	292	17	US-10-732-923-4816	Sequence 4805, Ap
42	128.5	9.6	349	14	US-10-115-571A-33	Sequence 4806, Ap
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44	128.5	9.6	383	17	US-10-732-923-4805	
45	128.5	9.6	383	17	US-10-732-923-4806	

ALIGNMENTS

RESULT 1
US-09-920-923-32
; Sequence 32, Application US/09920923
; Publication No. US20030022273A1
; GENERAL INFORMATION:
; APPLICANT: Teygenkov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/09/920,923
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 242
; TYPE: PRT
; ORGANISM: E-396
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-920-923-32

Query Match	100.0%	Score 1341	DB 10	Length 242
Best Local Similarity	100.0%	Pred. No. 4.4e-128		
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Gap 0				
QY	1	MSAHALPKADLTATSLIVSGGIIAAMLAHVLAFLDAAHPILAIVANFLGLTWSVGL	60	
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DB	61	FIHAHMGVSVGPGRANAAAGOLVLMVYGFSGWRKXIVZMAHRRAGTDDPDGPH	120	

OY		12	GGGVNVAARFICGFEGMRGGLLPVLTVTYATAMLDGRMYVFWPDLPSIIASIQLFVFGI	180
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OY		181	WLPHRPGHDAPDRHNARSRIISDPVSLTLCFHFQGYHHEHHLPPTYPMWRLPSTRTKGD	240
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OY		241	TA	242
Db		241	TA	242

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RESULT 2
US-10-166-225A-181
Sequence 181, Application US/10166225A
Publication No. US20030148416A1
GENERAL INFORMATION:
APPLICANT: BERRY, Alan
APPLICANT: BRETZEL, Werner
APPLICANT: HIMBELIN, Markus
APPLICANT: LOPEZ-OLIBARRI, Rual
APPLICANT: MAYER, Anne F.
APPLICANT: YEISEV, Alexei A.
TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REFERENCE: C38435/121966
CURRENT APPLICATION NUMBER: US/10/166,225A
CURRENT FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn version 3.1
SEQ ID NO 181
LENGTH: 242
TYPE: RPT
ORGANISM: Paracoccus carotinifaciens E-396
US-10-166-225A-181

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Query Match	100.0%;	Score 1341;	DB 14;	length 242;
Best Local Similarity	100.0%;	Pred. No. 4.4e-128;		
Matches 242;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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	MSAAALPKADLTATSLIVSGGIIAAMLAHVALMFLDAAAHPIIAVANFGLTWTLSVGL	60
Db	1 MSAAALPKADLTATSLIVSGGIIAAMLAHVALMFLDAAAHPIIAVANFGLTWTLSVGL	60
Qy	61 FIIANDMGSSVVRGSRPANAAMGQVLMLVAGFSMRKMIYKHNANHNNACTDDDPDRI	120
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Qy	181 WLPHRPGHDAPDRHNARSSRLSDPVSLITCFHFGUNHNENHNPVWWRILPSTRYKGD	240
	WLPHRPGHDAPDRHNARSSRLSDPVSLITCFHFGUNHNENHNPVWWRILPSTRYKGD	240
Db	181 WLPHRPGHDAPDRHNARSSRLSDPVSLITCFHFGUNHNENHNPVWWRILPSTRYKGD	240
Qy	241 TA 242	
	241 TA 242	
Db	241 TA 242	

RESULT 3
US-10-695-980-32
: Sequence 32, Application US/10695980
: Publication No US20040058410A1
: GENERAL INFORMATION:
: APPLICANT: Pasmontes, Luis
: APPLICANT: Teygankov, Yuri
: TITLE OR INVENTION: Fermentative Carotenoid Production
: FILE REFERENCE: 15464 US (C38435/125944)
: CURRENT APPLICATION NUMBER: US/10/695,980
: CURRENT FILING DATE: 2003-10-29

```

? PRIOR APPLICATION NUMBER: US/09/920,923B
? PRIOR FILING DATE: 2001-08-02
? PRIOR APPLICATION NUMBER: 08/980,832
? PRIOR FILING DATE: 1997-12-01
? NUMBER OF SEQ ID NOS: 66
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 32
? LENGTH: 242
? TYPE: PRT
? ORGANISM: Unknown
? FEATURE:
? OTHER INFORMATION: E-396
US-10-695-980-32

```

Query Match	100.0%;	Score 1341;	DB 15;	Length 242;
Best Local Similarity	100.0%;	Pred. No. 4.4e-128;		
Matches 242;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	MSAAALPKADLRATSLIYSGGIIIAAMLLAHYALWFLDAAHNPILAAVNFAGLTWLSVGL	60
Qy	MSAAALPKADLRATSLIYSGGIIIAAMLLAHYALWFLDAAHNPILAAVNFAGLTWLSVGL	60
Db	MSAAALPKADLRATSLIYSGGIIIAAMLLAHYALWFLDAAHNPILAAVNFAGLTWLSVGL	60
Qy	FIIAHDAAGSVVPGHPRANAAGQVLVLYLAGFSWRKMTIVKHAHNRHAGTDDDPDFH	120
Db	FIIAHDAAGSVVPGHPRANAAGQVLVLYLAGFSWRKMTIVKHAHNRHAGTDDDPDFH	120
Qy	GGVRRYAAFGIGYRCGRREGILLPIYIVVYALMIGDRMMVYFVWPLPSIIASIQLPFGI	180
Db	GGVRRYAAFGIGYRCGRREGILLPIYIVVYALMIGDRMMVYFVWPLPSIIASIQLPFGI	180
Qy	MLPBRGCHDAFPDRNHAAASRLSDPVSLLTCFHFQGYHNEHNLTPVPMWRLPSTRIKGD	240
Db	MLPBRGCHDAFPDRNHAAASRLSDPVSLLTCFHFQGYHNEHNLTPVPMWRLPSTRIKGD	240
Qy	TA 242	
Db	TA 242	

RESULT 4
US-10-997-844-33

```

: Sequence 33 Application US/10997844
: Publication No. US20050124033A1
: GENERAL INFORMATION:
: APPLICANT: Sharpe, Pamela L
: APPLICANT: Bosak, Melissa
: APPLICANT: Tao, Luan
: APPLICANT: Sedkova, Natalia
: APPLICANT: Cheng, Qiong L
: TITLE OF INVENTION: Optimized Bacterial Host Strains of Methylomonas sp. 16A
: FILE REFERENCE: CI-2230 US NA
: CURRENT APPLICATION NUMBER: US/10/597,844
: CURRENT FILING DATE: 2004-11-24
: PRIOR APPLICATION NUMBER: US 60/527,083
: PRIOR FILING DATE: 2003-12-03
: PRIOR APPLICATION NUMBER: US 60/527,877
: PRIOR FILING DATE: 2003-12-08
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 33
: LENGTH: 242
: TYPE: PRT
: ORGANISM: Agrobacterium aurantiacum
: US-10-997-844-33

```

Query Match	99.3%	Score 1331;	DB 18;	Length 242;
Best Local Similarity	98.8%	Pred. No. 4.6e-127;		
Matches 239; Conservative	2;	Mismatches 1;	Indels 0;	Gaps 0

Oy

I MSAAALPKADITATSLIVSGGIIAAMTALHVAALWFLDAAAHPILAVANFGLTWISVGL 60
				:				

Db

I MSAHALPKADITATSLIVSGGIIAAWTALHVAALWFDDAAAHPIILAIANFGLTWISVGL 60

Qy	61	FIADAHNGSVVPGPRANAAMGOLVWLXGFSNRKMIUKMAHNRHAGTDDDDPFI	120
Db	61	FIADAHNGSVVPGPRANAAMGOLVWLXGFSNRKMIUKMAHNRHAGTDDDDPFI	120
Qy	121	GGPVWVARFICTYFGWREGILLPVIVTVYALMLGDRMMYVVPWPLPSILASIQLFVFGI	180
Db	121	GGPVWVARFICTYFGWREGILLPVIVTVYALMLGDRMMYVVPWPLPSILASIQLFVFGI	180
Qy	181	WLPHPGHDAPFDRNANARSRIISDPVSLITCFHFGYHNEHHILAPVPPWRLPSTRTKGD	240
Db	181	WLPHPGHDAPFDRNANARSRIISDPVSLITCFHFGYHNEHHILAPVPPWRLPSTRTKGD	240
Qy	241	TA 242	
Db	241	TA 242	

```

RESULT 5
US-09-920-923-29
: Sequence 29, Application US/09920923
: Publication No. US20030022233A1
: GENERAL INFORMATION:
: APPLICANT: Pasamontes, Luis
: APPLICANT: Tsygankov, Yuri
: TITLE OF INVENTION: Improved Fermentative Carotenoid Production
: FILE REFERENCE: Improved Fermentative Carotenoid
: CURRENT APPLICATION NUMBER: US/09/920,923
: CURRENT FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: 08/980,832
: PRIOR FILING DATE: 1997-12-01
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO: 29
: LENGTH: 242
: TYPE: PRT
: ORGANISM: Alcaligenes PC-1
: US-09-920-923-29

```

RESULT 6
US-10-695-980-29
: Sequence 29, Application US/10695980
: Publication No. US20040058410A1
: GENERAL INFORMATION:
: APPLICANT: Pasamontes, Luis
: APPLICANT: Tsygankov, Yuri
: TITLE OF INVENTION: Fermentative Carotenoid Production
: FILE REFERENCE: 15464 US (C38435/125944)
: CURRENT APPLICATION NUMBER: US/10/695,980
: CURRENT FILING DATE: 2003-10-29
: PRIOR APPLICATION NUMBER: US/09/920,923B
: PRIOR FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: 08/980,832

```

; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.
; SEQ ID NO 29
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Alcaligenes PC-1
US-10-695-980-29

```

```

RESULT 7
US-10-466-656-39
; Sequence 39, Application US/10466656
; Publication No. US20040078846A1
; GENERAL INFORMATION:
; APPLICANT: desouza, Meryn L.
; APPLICANT: schreeder, William A.
; APPLICANT: Kollmann, Sherry R.
; APPLICANT: May, Colleen A.
; TITLE OF INVENTION: Carotenoid Biosynthesis
; FILE REFERENCE: 12794-004US1
; CURRENT APPLICATION NUMBER: US/10/466,656
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/288,984
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/264,329
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 244
; TYPE: prt
; ORGANISM: Brevundimonas aurantiaca
US-10-466-656-39

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Qy 12 TATSLLVSGGIIAAATLALHVALNF-----LDAANPLPLVAVANLGLTWISVGLFIAD 66
Dy 15 TWIGLTLAQMIVAGNAVLHVYGVVYHNRGRLPLTIVAPALVQ---TWISVGLFIAD 70
Qy 67 AMHGSAVPGRPRAANAAMGQULMLYAGSSNRKMTYKMAHHNRAGTDDPDRPHGCG--- 123
Dy 71 AMGSLAPRPRPLNAAVGRLTGLYAGRPRLTAAHHAAADAGTADDDFAPAPARAF 130
Qy 124 VRYTAAFIETYGMRGEGLLPLVITYVVALMLGDR-AMTVVFWPLPSLTIASIQLFVGVIML 182
Dy 131 LPPFLNFPRTTYGMRHMAVLTVLVALFGLGARPAULLFTMAAPALSLAQLFETGTWL 190
Qy 183 PRRPGDAFPDRNANASSRISDPVSLTLCFFHFGYTHHHHLHPVPPWRRL 232

Db 191 PRRHTDQFPADAHARSSGYPVLSLITCFHF-GRHHEHLSPWRPWRL 239

RESULT 8

US-10-848-307-39

/ Sequence 39, Application US/10848307

/ Publication No. US2005003474A1

/ GENERAL INFORMATION:

/ APPLICANT: desouza, Mervyn L.

/ APPLICANT: Schroeder, William A.

/ APPLICANT: Kollmann, Sherry R.

/ APPLICANT: May, Colleen A.

/ TITLE OF INVENTION: Carotenoid Biosynthesis

/ FILE REFERENCE: CGL00/0243US02

/ CURRENT APPLICATION NUMBER: US/10/848,307

/ CURRENT FILING DATE: 2004-05-18

/ PRIOR APPLICATION NUMBER: US 10/466,656

/ PRIOR FILING DATE: 2003-07-18

/ PRIOR APPLICATION NUMBER: US 60/288,984

/ PRIOR FILING DATE: 2001-05-04

/ PRIOR APPLICATION NUMBER: US 60/264,329

/ PRIOR FILING DATE: 2001-01-26

/ NUMBER OF SEQ ID NOS: 47

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 39

/ LENGTH: 244

/ TYPE: PRF

/ ORGANISM: Brevundimonas aurantiaca

US-10-848-307-39

Query Match 42.1%; Score 564; DB 17; Length 244;

Best Local Similarity 48.7%; Pred. No. 5.7e-49;

Matches 112; Conservative 28; Mismatches 76; Indels 14; Gaps 5;

QY 12 TATSLIVSGGIIAAMLAHVHLMF-----LDAAPHILAVANFLGLTSLVGLPIAND 66

Db 15 TWIGTLACMIYAGWAVHLYVGYFFRMGPRLTVIAPALVAVO---TWLSVGLPIVAND 70

QY 67 AHGSAVPRGRANAMGQLVLMVYAFSGMRKMTVMGMHHRHAGTDGDDPDHGP--- 123

Db 71 AMYGSIAFGRPRILNAAVGLTGLYAGFFRDLKTAHNAHNAAPGADDPDPAAPRAF 130

QY 124 VEWYARFIGTYFGWREGILLPVITVYALMLGDR-WMVVFWPPLPSIIASIQLFVFGIWL 182

Db 131 LPMFLNFFRTYFGWRMAVLTALVIALFGLGARPNLLTFWAAPALISALQLTFGTWL 190

QY 183 PRRGHDAFPRDHNAARSSRIDPVSLLTGFHFGYTHHHHLPYVWRL 232

Db 191 PRRHTDQFPADAHARSSGYPVLSLITCFHF-GRHHEHLSPWRPWRL 239

RESULT 9

US-09-791-687A-4

/ Sequence 4, Application US/09791687A

/ Patent No. US20020053096A1

/ GENERAL INFORMATION:

/ APPLICANT: Hirschberg, Joseph

/ APPLICANT: Lotan, Tamir

/ TITLE OF INVENTION: POLYNUCLEOTIDE MOLECULE FROM HAEMATOCOCCUS PLUVIALIS ENCODING A

/ TITLE OF INVENTION: POLYPEPTIDE HAVING A BETA-C-4-OXYGENASE ACTIVITY FOR BIOTECHNOLO

/ TITLE OF INVENTION: OF (3S,3'S) ASTAXANTHIN AND ITS SPECIFIC EXPRESSION IN CHROMOLA

/ FILE REFERENCE: 01/21600

/ CURRENT APPLICATION NUMBER: US/09/791,687A

/ CURRENT FILING DATE: 2001-02-26

/ PRIOR APPLICATION NUMBER: US 09/259,294

/ PRIOR FILING DATE: 1999-03-01

/ NUMBER OF SEQ ID NOS: 4

/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 4

/ LENGTH: 329

/ TYPE: PRF

/ ORGANISM: Haematococcus pluvialis

US-09-791-687A-4

Query Match 26.4%; Score 354.5; DB 9; Length 329;

Best Local Similarity 31.5%; Pred. No. 1.7e-27;

Matches 84; Conservative 44; Mismatches 104; Indels 35; Gaps 7;

QY 2 SAHALPKADLTATSLIVSGGIIAAMLAHVHLMF-----DAAAPHILA 46

Db 56 NAYKRPSPDGTGITWALR--VIGSWAVFLAIFQIKLPTSLDQLHMLPVSDATQOLVSG 113

QY 47 VAN-----FLGLTWLSVGLPIANDMHSVYVGRRAANAGQVLMLYAGFSWPKM 99

Db 114 TSSLIDIVVFVLEFLTYGLPIITTHDMHGILAMRNQLNDFGRVCISLYAMPDYMML 173

QY 100 IVKMAHHRHAG-TDDDPDHPGDP--VRMYARFIGTYFGWREGILLPVITVYALMLGD 156

Db 174 HRKWEHNNHTGEVAKDPDFHRGNPGIYVWFASSFSMSWQPARLAMWTVWQQLGAP 233

QY 157 RMWYVFWPPLPSIIASIQLFVFGIWLPHRP-----GHDAFPDRHNAARSSRIDPVSLL 209

Db 224 MANLLVFMAAPILISAFRLFYFGTYMPHKPBPAGASGSSPAVMMWWSKRTSQASDLVFL 293

QY 210 TCFHFGYTHHHHLPYVWRLPSTR 236

Db 224 TCYHF-DLHWERHRRWFPAPMWELPNCR 319

RESULT 10

US-10-310-154-466

/ Sequence 466, Application US/10310154

/ Publication No. US20030233670A1

/ GENERAL INFORMATION:

/ APPLICANT: Edgerton, Michael D

/ APPLICANT: Chomet, Paul S.

/ APPLICANT: Adams, Thomas H

/ APPLICANT: Ruff, Thomas G.

/ APPLICANT: Agarwal, Ameeta K.

/ APPLICANT: Ahrens, Jeffrey E.

/ APPLICANT: Ball, James A.

/ APPLICANT: Banu, G.

/ APPLICANT: Bell, Erin

/ APPLICANT: Boddupalli, Raghava

/ APPLICANT: Delkman, Jill

/ APPLICANT: Deng, Molian

/ APPLICANT: Dong, Jinzhuo

/ APPLICANT: Duff, Stephen M.

/ APPLICANT: Galligan, Meghan M.

/ APPLICANT: Hinchey, Brenda S.

/ APPLICANT: Huang, Shihshieh

/ APPLICANT: Johnson, G. Richard

/ APPLICANT: Jung, Vincent

/ APPLICANT: Kretzmer, Keith A

/ APPLICANT: Laccetti, Lucille B.

/ APPLICANT: Lai, Chao-Qiang

/ APPLICANT: Lee, Gary

/ APPLICANT: Lin, Jie-Yi

/ APPLICANT: Liu, Jindong

/ APPLICANT: Lu, Bin

/ APPLICANT: Luechy, Michael M.

/ APPLICANT: Lund, Adrian

/ APPLICANT: Madsen, Linda L.

/ APPLICANT: Malloy, Kathleen A.

/ APPLICANT: McKiel, Christine L.

/ APPLICANT: Miller, Philip W.

/ APPLICANT: Padmavathi, Nanchikanti

/ APPLICANT: Parnell, Laurence D.

/ APPLICANT: Start, William G.

/ APPLICANT: Tennessee, Dan

/ APPLICANT: Vidya, K.R.

/ APPLICANT: Wang, Haiyun

/ APPLICANT: Xin, Zhaunguo

/ APPLICANT: Xu, Nanfei

/ APPLICANT: Yang, Chunzhi

US-10-732-923-4730
Sequence 4730, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732, 923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310, 154
PRIOR FILING DATE: 2002-12-04

GenCore version 5.1.6,
Copyright (c) 1993 - 2005 CompuGen Inc.

OM protein - protein search, using sw model

Run on: June 17, 2005, 19:18:35 ; Search time 20.9423 Seconds

(without alignments)
1111.838 Million cell updates/sec

Title: US-10-695-980-32

Perfect score: 1341
Sequence: 1 MSAAHLPRKADLTATSLIVSG.....LHPTVPMWRLPSTRKGDPA 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	407.5	30.4	258	AF2204	beta-carotene keto
2	342.5	25.5	320	S65078	beta-carotene keto
3	190	14.2	685	C70678	probable electron
4	187.5	14.0	309	T31123	hypothetical prote
5	182	13.6	312	S77365	hypothetical prote
6	179.5	13.4	279	AB2307	hypothetical prote
7	158.5	11.8	345	T36617	probable Delta6 fa
8	152	11.3	369	S75038	hypothetical prote
9	143.5	10.7	329	D87673	conserved hypotet
10	135.5	10.1	350	S43772	phosphatidylcholin
11	135.5	10.1	350	AH2005	phosphatidylcholin
12	135.5	10.1	453	J02339	omega-3 fatty acid
13	135	10.1	424	JCS891	omega 6 desaturase
14	134	10.0	443	T01697	omega-3 fatty acid
15	131.5	9.8	398	T01697	omega-3 fatty acid
16	130.5	9.7	449	T50555	delta-8 sphingolip
17	130	9.7	449	AB4900	hypothetical prote
18	129.5	9.7	476	S52746	stearyl-CoA 9-des
19	128.5	9.6	383	T06238	omega-3 fatty acid
20	127	9.5	386	J02335	omega-3 fatty acid
21	126.5	9.4	287	T11959	fatty-acid desatur
22	126.5	9.4	351	S54259	Delta12 fatty acid
23	125.5	9.4	404	P00812	omega-3 fatty acid
24	125	9.3	377	J02337	omega-3 fatty acid
25	125	9.3	460	T10063	omega-3 fatty acid
26	123.5	9.2	381	T0323	probable Omega-3 f
27	122.5	9.1	359	S52650	omega-3 fatty acid
28	122	9.1	355	D95270	probable fatty aci
29	120.5	9.0	446	J02336	omega-3 fatty acid

30	119	8.9	438	2	T15039	omega-3 fatty acid
31	118.5	8.8	380	2	T06235	omega-3 fatty acid
32	118.5	8.8	380	2	J02338	omega-3 fatty acid
33	118	8.8	383	1	A44227	omega-3 fatty acid
34	116	8.7	347	2	S43771	phosphatidylcholin
35	116	8.7	451	1	J06180	stearyl-CoA 9-des
36	115	8.6	285	2	AG2429	delta-9 desaturase
37	114	8.5	376	2	J07871	stearyl-CoA 9-des
38	113.5	8.5	351	2	S11519	phosphatidylcholin
39	112.5	8.4	349	2	S43770	phosphatidylcholin
40	112.5	8.4	441	2	T03029	omega-3 fatty acid
41	111	8.3	352	2	B63901	fatty-acid desatur
42	110.5	8.2	449	2	T47950	delta-8 sphingolip
43	109	8.1	360	2	T32554	hypothetical prote
44	108	8.1	332	2	A85062	probable fatty aci
45	108	8.1	379	2	J02555	omega-3 fatty acid

ALIGNMENTS

RESULT 1

AF2204 beta-carotene ketolase [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #ext_change 09-Jul-2004

C/Accession: AF2204

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritaguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yaeuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

C/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AF2204

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-258 <KUR>

A/Cross-references: UNIPROT:O8YSA0; GB:BA000019; PIDN:BA074888.1; PID:G17132284; GSPDB:

C/Genetics:

A/Genes: alr3189

C/Superfamily: beta-carotene ketolase

Query Match 30.4%; Score 407.5; DB 2; Length 258;

Best Local Similarity 38.8%; Pred. No. 3.1e-29;

Matches 88; Conservative 39; Mismatches 87; Indels 13; Gaps 5;

QY 18 VSGIILAMWLALVHALWPL-----DAAPILAVANFLGLTWLSVGLFIADHMGCS 71

DB 27 INKGIFACFIPLFMALISLILSLIDTSIIHSLGLIAMLQTPYTGFIADHMGCV 86

QY 72 VVGRPRANAMGOLVLYIAGFSRKMTVKMAHNRNAGTDDPFDGCGV--WYA 128

DB 87 VPKPKPRINPFKGLTLILYGLLPIKMKMLHGHGTDLPDLYVNGHPQNFELWL 146

QY 129 RLIGTYFGMR--GLLPVTVTVALMLGDRMVVFWPPLSIASIOLEFVGIMLPHR 186

DB 147 HPMKSTWRKTQFLGLWM-IFHGLKVLVHLPENNLIIFMVPIISLSVOLFTGTFLPHK 205

QY 187 GHDAFPRNANRSRISPVSLITCFHFGHNEHNLHPTVPMWRLP 233

DB 206 LGGGTNPICARSIPLEFWSFVTCNF-GYKHEHVEYQQLPMWKL 251

RESULT 2

S65078 beta-carotene ketolase - Haematococcus pluvialis

C/Species: Haematococcus pluvialis

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #ext_change 09-Jul-2004

C/Accession: S65078

R/Kajiwa, S.; Kakizono, T.; Saito, T.; Kondo, K.; Ohtani, T.; Nishio, N.; Nagai, S.; M

Plant Mol. Biol. 29, 343-352, 1995

A/Title: Isolation and functional identification of a novel cDNA for astaxanthin biosynt

A:Reference number: S65078; MUID:96046752; PMID:7579184
 A:Accession: S65078
 A:Molecule type: mRNA
 A:Residues: 1-320 <KAJ>
 A:Cross-references: UNIPROT:Q39982; EMBL:D45881; NID:g1136638; P1DN:BA08300.1; P1D:dl00
 A:Experimental source: strain NIES-144
 A:Note: It is uncertain whether Met-1, Met-8 or Met-33 is the initiator
 C:Comment: This protein converts beta-carotene to canthaxanthin via echinenone. It may b
 C:Superfamily: beta-carotene ketolase

Query Match 25.5%; Score 342.5; DB 2; Length 320;
 Best Local Similarity 31.7%; Pred. No. 2.6e-23;
 Matches 84; Conservative 39; Mismatches 107; Indels 35; Gaps 8;

QY 3 AHALEKADLTATSLVSGGIIAAMLAHVHVL-----W-----FLDAA 40
 DB 48 AKRPASDAKGTMTALT--ITGTWAVFLHAIQRLPISMQLMPLPSEKTAOLGGS 105
 QY 41 AHPILAVANFLGLTWMISVGLFIADHMGSVVPRPRANAMGQLVIMLYAGFSMRKMI 100
 DB 106 SLSLHIAAVFIVLEFLYGLFITTDHMGHGTALHRRQNDLGNICISLVMFPYSMLH 165
 QY 101 VKHMAHNRAG-TDDPDPPDHGCP--VKRYAFICITGFMKREGLLPVITVYALMLGDR 157
 DB 166 RKGWHEHHNHTGVEGKDPFKKNPGLVFWFASFMSSYMSLWQFARLAWVAVMOMLGAPM 225
 QY 158 WMYVFWPLPSILASIQLFVFGIMLPHPR-----GHDAFPDRHARSRSIDPVSLLTC 211
 DB 226 ANLIVFMAAPILSAFLRFYFSTIYIPKREBPAGAGSQVMA-WFAKTSSEASDVMSFLTC 284
 QY 212 FHFGYVHHHHLPTVPMWRLPSTR 236
 DB 285 YHF-DLHWEHHRWPAFPMWQLPHCR 308

RESULT 3

C70678
 Probable electron transfer protein - Mycobacterium tuberculosis (strain H37Rv)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2004

C:Accession: C70678
 R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, J.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: C70678
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-685 <COJ>
 A:Cross-references: UNIPROT:P71946; GB:282098; GB:AL123456; NID:g3261664; P1DN:CA05067.
 A:Experimental source: strain H37Rv
 C:Genetics: fdxB
 C:Gene: fdxB
 C:Superfamily: Beta-carotene ketolase/phenylacetate metabolism ferredoxin reductase, etc
 C:Keywords: 2Fe-2S; metalloprotein
 F:617-671/Domain: ferredoxin [2Fe-2S] homology <FER>
 F:632,637/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 14.2%; Score 190; DB 2; Length 685;
 Best Local Similarity 26.4%; Pred. No. 2.7e-09;
 Matches 73; Conservative 38; Mismatches 98; Indels 68; Gaps 16;

QY 5 ALPK-----ADITAT--TSLIVSGGIIAAMLAHVHVLFLDAAAHPIAVANFLGLTW 55
 DB 43 ALPTGIFATLTAFGSTTAYISGW-IPFWYTI-----PVNAAVTVFV----- 84
 QY 56 LSVGLFIADHMGSVVPRPRANAMGQLVIMLYAG--FSRMRKIVYKMAHNRHAGTD 113
 DB 85 ---MFTVVDHSHVAISSIR-WVNGLFGRILA-WLFVGVAVPAFPGYTHIQHSHSDD 138

QY 114 D-DEP--FDHGG---PVRW-YANFIGYFGMRGGLLPVITV-----VYA 151
 DB 139 EODPDTFASHGSLWMLPLRMSMVEFYIKYLLPGRGRSPVIEVAVETLVMTLFLTLGLIVA 198
 QY 152 LMDGRMMYVFWPLPSILASIQLFVFGIMLPHPRGHDA-FPDHNRASSRIS-----DP 205
 DB 199 IVTGFWFLAVFLIPORIGTLVLAAMDWLPNHGLEBTPORSNNRYRATRNVRGAEWLFPT 258
 QY 206 VSLITCFHFGYVHHHHLPTVPMWRLPSTRKGDPA 242
 DB 259 VLSGQ-----NYHLVHHLHPSVPFPRYLRTRRNEEA 290

RESULT 4

T31123

hypothetical protein 15 - Sphingomonas aromaticivorans plasmid pNL1

C:Species: Sphingomonas aromaticivorans
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T31123
 R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.D.; Sisk, E.C.; Jensen, C.W.; G submitted to the EMBL Data Library, July 1998
 A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati.

A:Reference number: Z20992
 A:Accession: T31123
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-309 <ROM>
 A:Cross-references: UNIPROT:O85832; EMBL:AF079317; NID:g3378261; P1D:g3378264; P1DN:AAD0
 C:Genetics: plasmid pNL1
 A:Note: orf015
 C:Superfamily: beta-carotene ketolase

Query Match 14.0%; Score 187.5; DB 2; Length 309;
 Best Local Similarity 28.9%; Pred. No. 2e-09;
 Matches 77; Conservative 34; Mismatches 88; Indels 67; Gaps 17;

QY 5 ALPKADLTATSLVSGGIIAAM-LAH-VHAWFLDAAAHPIAVANFLGLTWISVGLFI 62
 DB 24 ALPTALFLVWSM---AGIATTWYALNLSMLPLM-----VGAISNGL-VTYL---LFS 68
 QY 63 IAHDMAGSV--VPRPRANAMGQLVIMLYAGFSMRKMIYKMAHNRHAGTDDPD--FD 119
 DB 69 VIHDSHKSLSVGINESIGAIQIFLFPAPAVMLRMV--HNKHHTHTGPKDPDFE 126
 QY 120 HGGPRWVARFLGTYFG-----W-----RSG--LT-----LPVITVYALMLGDRW 158
 DB 127 HESP-WMOVPRWTFDFGAYITWYFVYQONVRKKGTELVFYSLLVLFVAALYFGGW 185
 QY 159 MYVFWPLPSILASIQLFVFGIMLPHPRGHDAFPDRHNRASSRISDPVSLTFCFHG--- 215
 DB 186 ELFMFMFVPSRITLFLIIVFVILLPHNP-----AIIAODEDFV-MATTMRFGMEW 234
 QY 216 -----GYHHEHHLPTVPMWR 232
 DB 235 LNLPLVLYQNYHLHHLMPERIPFPRM 260

RESULT 5

S77365
 hypothetical protein s11468 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.
 A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: S77365

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S77365

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-312 <KAN>
 A:Cross-references: UNIPROT:P73428; EMBL:D90906; GB:AB001339; NID:G1652492; PIDN:BA1746
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Start codon: GTG
 C:Superfamily: beta-carotene ketolase

Query Match 13.6%; Score 182; DB 2; Length 312;
 Best Local Similarity 28.4%; Pred. No. 6.3e-09;

Matches 66; Conservative 41; Mismatches 71; Indels 54; Gaps 16;

QY 44 ILAVANFLGL-----TWISVGLFIIA-----HDAMGSAVPCPRANAMQCO---L 86
 DB 45 LMLAVAVFGWQWGLHMLHFCSCSVLAHLGTVIHDAHS-NAHNTIINAVLGHGSL 103
 QY 87 VLMVYGFSGKMKITVGMMAHHRHAGTDDDPDPH---GGPV-----RWYARITGYFG- 136
 DB 104 ML-----GFAFPVTRVYHLQHNAV-NDPENDPDHFVSTGRLFLIARFPYHEI-FFPKR 157
 QY 137 --WREGLLP-----VIVTVYALMLGDRMNVVF-----WPLSLIASIOLFPVGLMLPH 184
 DB 158 RLMRKYLELWELSRVLFTI--VFLGIRHGFIFGFWNTVFVPLVGLALGFLFDYLP 215
 QY 185 RPSGDAFPDRHNAASRISDPVSLITCFHFG-GYHHEHHLPTVPMWRPLST 235
 DB 216 RF-----FOERNRKNARVY-PSPLMLWLFQYNYHLHLHMLPSIPMYQYQNT 262

RESULT 6
 AB2307
 hypothetical protein alr4009 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AB2307
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MIMD:21595285; PMID:11759840
 A:Accession: AB2307
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-279 <KUR>
 A:Cross-references: UNIPROT:Q8YQ27; GB:BA000019; PIDN:BA875708.1; PID:G17133144; GSPDB:C
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: alr4009
 C:Superfamily: beta-carotene ketolase

Query Match 13.4%; Score 179.5; DB 2; Length 279;
 Best Local Similarity 28.6%; Pred. No. 9.4e-09;

Matches 68; Conservative 39; Mismatches 90; Indels 41; Gaps 17;

QY 16 LIVSGGIIAAMTALHVAHFLDAAHPIIAVANFLGLTWSGLFTIADAMGSAVPS 75
 DB 2 LIFSASVVMILITSNFGWLM---QMPHWLCFSTNTTALHCAGT---VINDACHQSAHRN 54
 QY 76 RPRANAMQCO---LVLMLVAGFSRKMIVGMMAHHRHAG-TDDDP--FDHGSPVWY-- 127
 DB 55 R-IINMMLGHGSLIL---AFAFPVTRVYHLQHNAVHNPXKDDPDHYVSTGRL-MLLA 108
 QY 128 ARFI--GTYFG---WREGLLP-----VIVTVYALMLGDRMNVV-FWPLPSLIASI 173
 DB 109 VRELVEVEFFQKRLMRKYLELWELSRVLFTIIVITIVISVQYHFLGYILNFWFIPAFIVGI 168
 QY 174 QLVFVGLTWLPHRSGDAFPDRHNAASRISDPVSLITCFHFG-GYHHEHHLPTVPMW 230
 DB 169 ALGLFDYLPYHRP---FVERDRWKARVY-PGKLNLILMIGQNYHLHLHMLPSIPMY 221

RESULT 7

T36617
 Probable Delta6 fatty acid desaturase (EC 1.14.99.-) SCH35.42c [similarity] - Streptomyces
 C:Species: Streptomyces cellcolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T36617
 R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, June 1999
 A:Reference number: Z21610
 A:Accession: T36617
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-345 <OLI>
 A:Cross-references: UNIPROT:Q9X8W4; EMBL:AL078610; PIDN:CA844385.1; GSPDB:GN00070; SCOE
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SCH35.42c
 C:Superfamily: fatty acid desaturase/sphingolipid desaturase
 C:Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match 11.8%; Score 158.5; DB 2; Length 345;
 Best Local Similarity 27.2%; Pred. No. 8.9e-07;

Matches 74; Conservative 32; Mismatches 83; Indels 83; Gaps 18;

QY 18 VSGGIIAAMLA-LHYVALFELDAAHPIIAVANFLGLTWLSGLFTIADAMGSAVPCR 76
 DB 44 VTGLVYAGMAAFVLYGASWV-----TLAIAFLAVMYGOVAL--VAHDMARQVF-RR 93
 QY 77 PRANAMQGLVIMLYAGFS-----WRKMIVGMMAHHRHAGTDD-DPPF-----D 119
 DB 94 RRASELSGRI-----AGASIGMSYGMQD--KTRRHANPNTEDIDPDIGDPLVWSPD 145
 QY 120 HGGPVWYVRFITGYGMEGLLPVIVV-----YALMLGD 156
 DB 146 QARAAATGLPRLGR---WQAFIFPRLITEGNMYVYASGRAMNRRLKRALDGLLH 202
 QY 157 RMYTV--VEMPLPSILA-----SIOLFVFGIWT--PHRPGH-----DAFPD--RHNR 198
 DB 203 CAVYTLALFMVLPFGMAIAFLAVHQLCFVYLGSAFAFHKGMPIITADDRPDLRQVL 262
 QY 199 SSRISDPVSLITCFHFGYTH--EHHHLPTV 228
 DB 263 TSRNVNG-GLFTDLALGSLHQLIENHLFSPSP 293

RESULT 8

S75038
 hypothetical protein sll1611 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: S75038
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 A:Reference number: S74322; MIMD:97061201; PMID:8905231
 A:Accession: S75038
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-369 <KAN>
 A:Cross-references: UNIPROT:P73843; EMBL:D90910; GB:AB001339; NID:G1652956; PIDN:BA1790
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Genetics:
 A:Start codon: GTG

Query Match 11.3%; Score 152; DB 2; Length 369;
 Best Local Similarity 26.4%; Pred. No. 3.6e-06;

Matches 77; Conservative 27; Mismatches 84; Indels 104; Gaps 19;

QY 16 LIVSG---GIIAAMT--ALHVAH-----LM-FLDAAHPIIAVANFLGLTWSGLFTI- 63
 DB 28 LVILGILGIVYAGLTIARHLHQPQWMLFLPMA-----LIMGN-----SVTVFLFG 76

RESULT 13
JC5891
omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtii
C.Species: Chlamydomonas reinhardtii
C.Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 09-Jul-2004
C.Accession: JC5891
R.Saco, N.; Fujiwara, S.; Kawaguchi, A.; Tsunuki, M.
J. Biochem. 122, 1224-1232, 1997
A.Title: Cloning of a gene for chloroplast omega 6 desaturase of a green alga, Chlamydomonas reinhardtii
A.Reference number: JC5891, MUID:98158334, PMID:9498569
A.Accession: JC5891
A.Status: nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-424 <SAT>
A.Cross-references: UNIPROT:O46663; DDBJ:AB007640; NID:92666716; PIDN:BA23881.1; PID:92666716
C.Comment: This enzyme catalyzes the desaturation of monoenoic to dienoic acids.
C.Genetics:
A.Gene: des6
C:Superfamily: fatty acid (acyl-CoA) desaturase

Query Match 10.0%; Score 134; DB 2; Length 443;
 Best Local Similarity 23.3%; Pred. No. 0.00018;
 Matches 69; Conservative 32; Mismatches 99; Indels 96; Gaps 17;

```

OY      21 GIATMALATHALWFLD---AAAHPIAAVNFGLT-----WLSVG--- 59
Db      95 GLAIRAIPRG-C-WYXDPWRMSWYLRDVAVVGLLAAARALDLSWLPWLYMAAQGTF 153
OY      60 --LFIITADAHGSSVVGPRPRANAAGOL-----VLMYAGSPKMKIIVKHAHHRHAGTD 113
Db      154 WALTVVLGHDGCHG-SFNNPKLNSVVGHIHSSILVPHG--WR--ISHRTTHQNHGV 207
OY      114 DDPPFDHGGPRKMT-----ARFT-----GTYGKMEGLLP 144
Db      208 EKDSWMPRLPRKLYKSLDFMTKRLKFLTWPPLAFPLYLFAKSPGKSGSHNPQSDLFOP 267
OY      145 V-----IYTVVAYLMYGRWYVV-----FWPLPSI-LASIQLFVFGIWL-----HR 185
Db      268 TEKDDIITSTA-----SWLAAVVGVLAGITFLMGVLPMTKLGVPYLVFVAALDWIYLYHH 322
OY      186 PGH-DAFPPDRINNAASSRISDPVSL-----TCFPHGGVHHHHHHHPYAPPMWR 232
Db      323 HGHDDKLPWTRGKEMWYLRGLGTLTLDKDYGMINNHHIDIGHVYVHHLPQIPIYH 378

```

RESULT 15

T01696

omega-3 fatty acid desaturase (EC 1.14.99.-) FAD8 - maize (fragment)

C:Species: Zea mays (maize)

C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004

C:Accession: T01696

R:Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.; Kusano, T.

Plant Mol. Biol. 36, 297-306, 1998

A:Title: Two maize genes encoding omega-3 fatty acid desaturase and their differential e

A:Reference number: Z14400; M0ID:98145435; PMID:9484441

A:Accession: T01696

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-398 <BER>

A:Cross-references: UNIPROT:Q24626; EMBL:D33953; NID:G2446995; PIDN:BA22440.1; PID:G244

A:Experimental source: strain honey bantum

C:Gene: FAD8

C:Genetics:

C:Superfamily: fatty acid (acyl-CoA) desaturase

C:Keywords: oxidoreductase

Query Match

9.8%; Score 131.5; DB 2; Length 398;

Best Local Similarity 24.1%; Pred. No. 0.00027;

Matches 67; Conservative 30; Mismatches 98; Indels 83; Gaps 15;

```

QY 16 LTVSGGIIAAWALAHVHALMPLDAAHPIAVANFLGLTWTLSVGLPTIAHDAMHGSVVP 75
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 78 VVVVVLGLAAARLDSWLVWPLYMAQGT-----MFW---ALFVLGHDCGHS-FSN 125
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 76 RPRANAAMGOL---VLMVYAGFSWRKMTVKMAHHRHAGTDDPDFDHGSPVRY---- 127
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 126 NPKLMSVVGHIILHSSILVYHG--WR---ISHRTHQNNGHYEKESWHPLEPLKSLD 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 128 -----ARFI-----GTFGMRGGLLP---VITYTVALMLGDRW 158
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 FMTRKLRFTMPPEPLAFLPLPARSPKSGSHFNPSDDLFOPNKKDITSTA-----SW 235
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 159 MVVV-----FWPLPSI-LASIQLFVEGIWLP-----HRPGH-DAFPDRHNAASSRI 202
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 LAMVGVLAGLTFLMGFVAMLKLVGPYFVFAVMDNVTYLRHHGHEDKLPWTRGOEWSYL 295
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 203 SDPVSL-----TCFHFGYHHEHHLAPTVPMWRL 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 296 RGGITTLDRDXGLINNHHIDIGHVTHHLFPQIPHYHL 333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: June 17, 2005, 19:38:05

Job time : 21.9423 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2005, 18:55:34 ; Search time 91.1378 Seconds

(without alignments)
1359.734 Million cell updates/sec

Title: US-10-695-980-32

Perfect score: 1341

Sequence: 1 MSAAHLPKADLTATSLIVSG.....LHPTVPMRLPSTRKGDRA 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1332	99.3	242	2 CRTW_AGRAU	Q9RLH7 paracoccus
2	1331	99.3	242	1 CRTW_AGRAU	P54972 algalbacteri
3	1044	77.9	242	1 CRTW_AGRAU	Q44261 algalbacteri
4	600	44.7	258	2 Q9K1X0	Q9K1X0 bradyrhizob
5	570	42.5	244	2 Q8GCT5	Q8GCT5 brevundimon
6	424.5	31.7	257	2 Q7NJV4	Q7NJV4 glacobacter
7	407.5	30.4	258	2 Q8VSA0	Q8VSA0 anabaena sp
8	406.5	30.3	229	2 Q847D1	Q847D1 nodularia s
9	359	26.8	244	2 Q7U6H0	Q7U6H0 synecococc
10	354.5	26.4	339	2 Q23973	Q23973 haematococc
11	350.5	26.1	320	1 Q6J3N5	Q6J3N5 haematococc
12	342.5	25.5	320	1 CRTW_HAEPL	Q39982 haematococc
13	300.5	22.4	276	2 Q8LJQ2	Q8LJQ2 haematococc
14	194.5	14.5	344	2 Q7UDV2	Q7UDV2 prochlorococ
15	190	14.2	672	2 Q7D5A7	Q7D5A7 mycobacteri
16	190	14.2	685	2 P71846	P71846 mycobacteri
17	190	14.2	685	2 Q7TW80	Q7TW80 mycobacteri
18	189	14.1	343	2 Q7U9G7	Q7U9G7 synecococc
19	187.5	14.0	309	2 Q8S832	Q8S832 sphingomonas
20	187	13.9	325	2 Q8DHP5	Q8DHP5 synecococc
21	182	13.6	312	2 P73428	P73428 synecococc
22	179.5	13.4	279	2 Q8YQ27	Q8YQ27 anabaena sp
23	167	12.5	346	2 Q7V4X0	Q7V4X0 prochlorococ
24	159.5	11.9	283	2 Q7NCM0	Q7NCM0 glacobacter
25	158.5	11.8	345	2 Q9X8M4	Q9X8M4 streptomyc
26	152	11.3	359	2 P73843	P73843 streptomyc
27	148	11.0	379	2 Q6LJB6	Q6LJB6 photobacter
28	146.5	10.9	340	2 Q981L0	Q981L0 rhizobium 1
29	145	10.8	355	2 Q6N9E6	Q6N9E6 rhodospseudo
30	143.5	10.7	329	2 Q9A2Y4	Q9A2Y4 caulobacter
31	143.5	10.7	493	2 Q89T03	Q89T03 bradyrhizob

32	143	10.7	327	2 Q52580	Q52580 pseudomonas
33	141	10.5	584	2 Q52468	Q52468 pseudomonas
34	139	10.4	298	2 Q8PMP8	Q8PMP8 xanthomonas
35	139	10.4	301	2 Q8XRN9	Q8XRN9 raietonia s
36	139	10.4	341	2 Q8GGR8	Q8GGR8 streptomyc
37	139	10.4	350	2 Q704F1	Q704F1 noscoc sp.
38	138.5	10.3	465	2 Q7S1A7	Q7S1A7 neurospora
39	138	10.3	349	2 Q8PAZ4	Q8PAZ4 xanthomonas
40	136	10.1	320	2 Q6N921	Q6N921 rhodospseudo
41	135.5	10.1	350	2 Q79F72	Q79F72 anabaena va
42	135.5	10.1	350	2 Q44503	Q44503 anabaena sp
43	135.5	10.1	453	1 FD3C_SOYBN	FD3C_SOYBN max
44	135	10.1	424	2 Q48663	Q48663 chlamydomon
45	134	10.0	327	2 Q82S54	Q82S54 nitrosomona

ALIGNMENTS

RESULT 1

ID	Q9RLH7	PRELIMINARY	PRT	242 AA.
AC	Q9RLH7	01-MAY-2000 (TREMblrel. 13, Created)		
DT	01-MAY-2000 (TREMblrel. 13, Last sequence update)			
DT	01-MAR-2004 (TREMblrel. 26, Last annotation update)			
DE	Beta-carotene C-4-oxygenase (Ketolase).			
GN	Name=crw;			
OS	Paracoccus marcusii.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;			
OC	Rhodobacteriaceae; Paracoccus.			
OX	NCBI_TaxID=59779;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=WH1;			
RA	Harker M., Hirschberg J.,			
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; Y15112; CAB56059.1; -			
DR	GO; GO:0016701; F:oxidoreductase activity, acting on single d. . .; IEA.			
DR	GO; GO:0016119; F:carotene metabolism; IEA.			
DR	InterPro; IPR011393; Carotene_ketolas.			
DR	InterPro; IPR010257; Carotene_ketolas.			
DR	Pfam; PF00487; FA_decatase sub.			
DR	PIRSF; PIRSF027840; Carotene_ketolas; 1.			
DR	ProDom; PD001061; FA_decat sub; 1.			
SQ	SEQUENCE 242 AA; 27114 MW; 5D98AD16412416C2 CRC64;			

Query Match 99.3%; Score 1332; DB 2; Length 242;
Best local Similarity 99.2%; Pred. No. 2.3e-110;
Matches 240; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1 MSAAHLPKADLTATSLIVSGGIIAAMLAHVAFDAAHPILAANFLGILTWISVGL	60
DB	1 MSAAHLPKADLTATSLIVSGGIIAAMLAHVAFDAAHPILAANFLGILTWISVGL	60
QY	61 FIIADHMGSVPRPRANAMGQVLMVYGFSGFRKIVYGMHHRAGDDDDPDH	120
DB	61 FIIADHMGSVPRPRANAMGQVLMVYGFSGFRKIVYGMHHRAGDDDDPDH	120
QY	121 GGPVRYAFICGYFGMRGGLLPVIVTVYVLMGDRWYVFWPLPSILASIQLFVFT	180
DB	121 GGPVRYAFICGYFGMRGGLLPVIVTVYVLMGDRWYVFWPLPSILASIQLFVFT	180
QY	181 WIPHRGHDAPDRNNAASRISDPVSLTCTHFGYTHHHLLPVPWRLPSTRKCD	240
DB	181 WIPHRGHDAPDRNNAASRISDPVSLTCTHFGYTHHHLLPVPWRLPSTRKCD	240
QY	241 TA 242	
DB	241 TA 242	

```

RESULT 2
ID_CRTW_AGRAU STANDARD; PRT; 242 AA.
AC P54972;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Beta-carotene ketolase (EC 1.13.-.-) (Beta-carotene oxygenase).
OS Name=crtw;
OS Agrobacterium aurantiacum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=41455;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96062243; PubMed=7592436;
RA Misawa N., Satomi Y., Kondo K., Yokoyama A., Kajiwara S., Salto T.,
RA Ohtani T., Miki W.;
RT "Structure and functional analysis of a marine bacterial carotenoid
RT biosynthesis gene cluster and astaxanthin biosynthetic pathway
RT proposed at the gene level."
RT J. Bacteriol. 177:6575-6584(1995).
CC -!- FUNCTION: Converts beta-carotene to canthaxanthin via echinenone.
CC -!- PATHWAY: Carotenoid biosynthesis. Involved in astaxanthin
CC biosynthetic pathway.
-----
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DR EMBL; D58420; BA09591.1; -
DR InterPro; IPR005804; FA_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF027840; Carotene ketolase; 1.
DR Prodom; PD001081; FA_desat_sub; 1.
KW Carotenoid biosynthesis; Oxidoreductase.
SQ SEQUENCE 242 AA; 27128 MM; 6AEBB5BF60BE3D6B CRC64;

Query Match 99.3%; Score 1331; DB 1; Length 242;
Best Local Similarity 98.8%; Pred. No. 2.8e-110;
Matches 239; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSAAALPKADLTSTLSIVGGITAAALAHVHALWFLDAAAPILAVANLGLTWLSVGL 60
DB 1 MSAAALPKADLTSTLSIVGGITAAALAHVHALWFLDAAAPILAVANLGLTWLSVGL 60
QY 61 FTIAHDAMGVSVPGRPRANAAGOLVLMVYAGFSWRKMIIVKMAHRRHAGTDDDDPDH 120
DB 61 FTIAHDAMGVSVPGRPRANAAGOLVLMVYAGFSWRKMIIVKMAHRRHAGTDDDDPDH 120
QY 121 GGPVRYAFAFGTYFGMRBGLLPVIVTYAALADPRMYVVFVWPLPSILASIQLFVFGT 180
DB 121 GGPVRYAFAFGTYFGMRBGLLPVIVTYAALADPRMYVVFVWPLPSILASIQLFVFGT 180
QY 181 WLPHRFGHDAFPDRHNAARSRIISDPVSLTTCFHFSGYHHEHHLAPVPMWRLLPSTTKGD 240
DB 181 WLPHRFGHDAFPDRHNAARSRIISDPVSLTTCFHFSGYHHEHHLAPVPMWRLLPSTTKGD 240
QY 241 TA 242
DB 241 TA 242

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Beta-carotene ketolase (EC 1.13.-.-) (Beta-carotene oxygenase).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95251715; PubMed=7733978;
RA Misawa N., Kajiwara S., Kondo K., Yokoyama A., Satomi Y., Salto T.,
RA Miki W., Ohtani T.;
RT "Canthaxanthin biosynthesis by the conversion of methylene to keto
RT groups in a hydrocarbon beta-carotene by a single gene."
RT Biochem. Biophys. Res. Commun. 209:867-876(1995).
CC -!- FUNCTION: Converts beta-carotene to canthaxanthin via echinenone.
CC -!- PATHWAY: Carotenoid biosynthesis. Involved in astaxanthin
CC biosynthetic pathway.
-----
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CC or send an email to license@isb-sib.ch).
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DR EMBL; D58422; BAA09596.1; -
DR InterPro; IPR005804; FA_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF027840; Carotene ketolase; 1.
DR Prodom; PD001081; FA_desat_sub; 1.
KW Carotenoid biosynthesis; Oxidoreductase.
SQ SEQUENCE 242 AA; 26939 MM; 077DA83FAAD14E4 CRC64;

Query Match 77.9%; Score 1044; DB 1; Length 242;
Best Local Similarity 77.5%; Pred. No. 9e-85;
Matches 179; Conservative 17; Mismatches 35; Indels 0; Gaps 0;

QY 12 TATSLIVGGITAAALAHVHALWFLDAAAPILAVANLGLTWLSVGLFTIAHDAMGVS 71
DB 12 TATSLIVGGITAAALAHVHALWFLDAAAPILAVANLGLTWLSVGLFTIAHDAMGVS 71
QY 72 VVPGPRANAAGOLVLMVYAGFSWRKMIIVKMAHRRHAGTDDDDPDHGGPVRYAFAFI 131
DB 72 VVPGPRANAAGOLVLMVYAGFSWRKMIIVKMAHRRHAGTDDDDPDHGGPVRYAFAFI 131
QY 132 GTYFGMRBGLLPVIVTYAALADPRMYVVFVWPLPSILASIQLFVFGITWLPHRFGHDAF 191
DB 132 GTYFGMRBGLLPVIVTYAALADPRMYVVFVWPLPSILASIQLFVFGITWLPHRFGHDAF 191
QY 132 STYFGMRBGLLPVIVTYAALADPRMYVVFVWPLPSILASIQLFVFGITWLPHRFGHDAF 191
DB 132 STYFGMRBGLLPVIVTYAALADPRMYVVFVWPLPSILASIQLFVFGITWLPHRFGHDAF 191
QY 192 PDRHNAARSRIISDPVSLTTCFHFSGYHHEHHLAPVPMWRLLPSTTKGDTA 242
DB 192 PDRHNAARSRIISDPVSLTTCFHFSGYHHEHHLAPVPMWRLLPSTTKGDTA 242

RESULT 4
ID_O9KIX0 PRELIMINARY; PRT; 258 AA.
AC O9KIX0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Beta-carotene ketolase.
OS Name=crtw;
OS Bradyrhizobium sp. ORS278.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=114615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORS278;

```



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RX MEDLINE=20309720; PubMed=10851005;
RA DOI=10.1128/JB.182.13.3850-3853.2000;
RA Hamibai L., Lorguin J., Angles d'Orcoli N., Garcia N.,
RA Chahtreul C., Masson-Boivin C., Dreyfus B., Girard E.,
RA "Isolation and characterization of the canthaxanthin biosynthesis
RT genes from the photosynthetic bacterium Bradyrhizobium sp. strain
RT ORS778. "
RL J. Bacteriol. 182:3850-3853 (2000).
DR EMBL, AF218415; AAF78203.1; -.
DR GO; GO:0016701; F:oxidoreductase activity, acting on single d. .; IEA.
DR GO; GO:0016119; P:carotene metabolism; IEA.
DR InterPro; IPR011393; Carotene ketolase.
DR InterPro; IPR005804; Fa_desat.
DR InterPro; IPR010257; Fa_desat_sub.
DR Pfam; PF00487; Fa_desaturase; 1.
DR PIRSF; PIRSF027840; Carotene ketolase; 1.
DR Prodom; PD001081; Fa_desat_sub; 1.
SQ SEQUENCE 258 AA; 29736 MW; 4C0819FC30465D0 CRC64;

Query Match 44.7%; Score 600; DB 2; Length 258;
Best Local Similarity 49.6%; Pred. No. 2.8e-45;
Matches 113; Conservative 35; Mismatches 74; Indels 6; Gaps 4

OY LIVSGGIIAAMTLAHLVHLMFLDAAHPILAANFLGL-TWLSVGLFIADAHGSSVP 74
Db LTLAAVITAAMLVHVGAMLFEPRLTILSHLPLVLTQTLVYGLFIADAHGSSLPV 85
OY GRPANAAMGOLVLMVLVGFSPKMKIVKMAHHRHAGTDDEDPDHGDP--VRYARFI 131
Db FKQVNRIRIGQLCLFLVYGFSPDALNVEHKKHRRRGTAEDDPDEVPHGWMFASPF 145
OY 132 GTYFGRBGLLPIVTVYVYATMLGDRMKT-VFWLPLSLASIQLFVGIWLPHPRGDA 190
Db LHFEKMKQVAAIIAAVSLVYQVLFAPVPLQNTILFMPLPGLISALQTFEGTYLPHKPAQ 205
OY 191 FPDNRNASSRISDPVSLITCPHCGYHHEHHLHPMPWRLPSPRTK 238
Db FADNRNARTSEFPAMLSLTCFHP-GFHHHHLHPDAPWWRLPETIKR 252

RESULT 5
O8GCTS PRELIMINARY; PRT; 244 AA.
AC O8GCTS;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Beta-carotene C4 oxygenase.
GN Name=ctfW;
OS Brevundimonas aurantiaca.
OC Bacteriia; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
OC Caulobacteraceae; Brevundimonas.
OX NCBI_TaxID=74316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15266;
RA de Souza M.L., Kollmann S.R., Schroeder W.A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBD databases.
DR EMBL: AY166610; AAN6030.2; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; Fa_desat.
DR InterPro; IPR010257; Fa_desat_sub.
DR Pfam; PF00487; Fa_desaturase; 1.
DR Prodom; PD001081; Fa_desat_sub; 1.
SQ SEQUENCE 244 AA; 27261 MW; 17857874433819DA CRC64;

Query Match 42.5%; Score 570; DB 2; Length 244;
Best Local Similarity 49.1%; Pred. No. 1.2e-42;
Matches 113; Conservative 27; Mismatches 76; Indels 14; Gaps 5

OY 12 TATSLIVSGGIIAAMTLAHLVHLMF-----LDAAHPILAANFLGLTWLSVGLFIAD 66
Db 15 TWIGTLGLAMTVAGNAVLVGVVYFHRMGRLTLVTAIPALVAQ---TWLSVGLFIAD 70

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[illegible]

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ID Q8YSA0 PRELIMINARY; PRT; 258 AA.
AC Q8YSA0;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta-carotene ketolase.
GN OrderedLocusNames=AI13189;
OC Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Molk C.P., Sasamoto S.,
RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003592; BAB74888.1; -.
DR PIR; AP0204; AF2204.
DR GO; GO:0016701; F:oxidoreductase activity, acting on single d. .; IEA.
DR GO; GO:0016119; P:carotene metabolism; IEA.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF027840; Carotene ketolase; 1.
DR ProDom; PD001081; FA_desat_sub; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 30313 MW; 8F6C8E4ECF8E61B CRC64;

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Query Match 30.4%; Score 407.5; DB 2; Length 258;
Best Local Similarity 38.8%; Pred. No. 3.6e-28;
Matches 88; Conservative 39; Mismatches 87; Indels 13; Gaps 5;

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QY 18 VSGGIIAAMLAHVHLMFL-----DAAPHLAVANFLGTLTWSVGFIAHDAMGCS 71
DB 27 INKGIFACIFILFWAISLILSLIDTSIIHKSLGIALMOTFLYGLFIRAHAMGV 86
QY 72 VVPGPRPRAAAMGOLVLMYAGFSWRKMI VKMAHHRHGHTDDPDHFGVPR--WYA 128
DB 87 VVPGPRPRAAAMGOLVLMYAGFSWRKMI VKMAHHRHGHTDDPDHFGVPR--WYA 146
QY 129 REIGTYFGWR--GLLLPVITVYALMLGDRMYVFWPPLPSILASIQLFVGVMLPHRP 186
DB 147 HFMKSYWRTQIFGLWM-IFHGLKULVHIPPENLLIFMWPISILSVQFYGTFLPHK 205
QY 187 GHDAPPDRNARSSRIDPVSLITCFHGGYHHEHHLPTVPMWRLP 233
DB 206 LBGYTNPHCARSIPLFLFMSFVTCYHF-GYHKEHHEYPQLPMMWKL 251

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RESULT 8
ID Q847D1 PRELIMINARY; PRT; 229 AA.
AC Q847D1;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative beta-carotene ketolase.
OS Nodularia spumigena.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nodularia.
OX NCBI_TaxID=70799;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NSOR10;
RX MEDLINE=22549861; PubMed=12664164; DOI=10.1007/s00239-002-2415-0;
RA Moffett M.C., Neilan B.A.;
RT "Evolutionary affiliations within the superfamily of ketosynthases
RT reflect complex pathway associations.";
RL J. Mol. Evol. 56:446-457(2003).
DR EMBL; AJ210783; AA064399.1; -.
DR GO; GO:0016701; F:oxidoreductase activity, acting on single d. .; IEA.

```

```

DR GO; GO:0016119; P:carotene metabolism; IEA.
DR InterPro; IPR011593; Carotene ketolase.
DR InterPro; IPR005804; Fa_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF027840; Carotene ketolase; 1.
DR ProDom; PD001081; FA_desat_sub; 1.
SQ SEQUENCE 229 AA; 27832 MW; 71C9271BB371C95B CRC64;

```

```

Query Match 30.3%; Score 406.5; DB 2; Length 229;
Best Local Similarity 38.4%; Pred. No. 3.9e-28;
Matches 86; Conservative 41; Mismatches 76; Indels 21; Gaps 9;

```

```

QY 22 IIAAWLALHVALHLMFLDAAPHT-LAVANFLGLTWLSVGLFIIADAMGSGVPRPRAN 80
DB 5 IISIV-AISLGLIYIDISQPKFWMLLPLIFMQFELYGLFITYHADAMHGVFPKPKIN 63
QY 81 AAMGOLVLMYAGFSWRKMI VKMAHHRHGHTDDPDHFGVPR--WYARPGTYFG 136
DB 64 HFIGSLCLFLYGLLPYQKLKKHMLHHNPASETPDF-HNGKQKNFPAWLYFMRKYS 122
QY 137 WREGLLPVITVYALMLGDRMY-----VFWPPLPSILASIQLFVFGIMLPHPRGHDAF 191
DB 123 WLGITLWITLYNLKTI-----WHRPEDMNTYFWVVPISLSIQLFYGTFLPHSPVGCY 178
QY 192 PDRNARSSRIDPV--SLITCFHGGYHHEHHLPTVPMWRLP 233
DB 179 KEPP--RSQTISRPIWMSFITCYHF-GYHKEHHEYPVPMWQLP 219

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RESULT 9
ID Q7U6H0 PRELIMINARY; PRT; 244 AA.
AC Q7U6H0;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Possible beta-carotene ketolase.
GN OrderedLocusNames=SYMW1368;
OS Synechococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahamsa B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarron J.,
RA Paulsen I.T., Dufrene A., Patteny F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569692; CAB07883.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; Fa_desat.
DR InterPro; IPR010257; FA_desat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_sub; 1.
KW Complete proteome.
SQ SEQUENCE 244 AA; 27434 MW; 77A71180F75875B7 CRC64;

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Query Match 26.8%; Score 359; DB 2; Length 244;
Best Local Similarity 36.2%; Pred. No. 7e-24;
Matches 85; Conservative 41; Mismatches 97; Indels 12; Gaps 7;

```

```

QY 16 IIVSGIIAAMLAHVHLMFLDAAPHT-LAVANFLGLTWLSVGLFIIADAMGSGVPR 74
DB 13 IALAGLISAWL-LSLGSITPLDQTPGLIGSLILRALFLHGLFIVAHDSPASLAVP 71
QY 75 GPRPANAAMGOLVLMYAGFSWRKMI VKMAHHRHGHTDDPDHFGVPR--HGPVRYAFPI 131
DB 72 GHPGILNRWIGKVVLLVYAGLSYERCSRHRHHLAETFPQDPDQRCNNNNIILWYVFM 131
QY 132 GTYFGMRGGLLPVITVYALMLGCD---RMNY-VFWPPLPSILASIQLFVFGIMLPHP 186

```

Db 132 GNYLGRQOLNLSCLMIALIILNGSDLPADQIMHLLFSVLPILISSCOLFLVGTWLPFHR 191

QY 187 GHDAFDRNRNASSRSDPSVSLTCHFGCYHHEHLLHPVWRRLPSTRKCDT 241

Db 192 GATTRG-VTTRSLALPALSPACYNF-GYRHHHSBSTPWFQOLPQINESFT 244

RESULT 10

023973 PRELIMINARY; PRT; 329 AA.

AC 023973; 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DB Beta-carotene C-4 oxygenase (Ketolase).

GN Name=Cito;

OS Haematococcus pluvialis.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Haematococcaceae; Haematococcus.

OX NCBI_TaxID=44745;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=34/7;

RX MEDLINE=97227932; PubMed=9119049; DOI=10.1016/S0014-5793(97)00110-5;

RA Harker M., Hirschberg J.;

RT "Biosynthesis of ketocarotenoids in transgenic cyanobacteria expressing the algal gene for Z-C-4-oxygenase, Cito.";

RL FEBS Lett. 404:129-134(1997).

DR EMBL; X86782; CAA60478.1; -

DR GO; GO:0016701; P:oxidoreductase activity, acting on single d. .; IEA.

DR GO; GO:0016119; P:carotene metabolism; IEA.

DR InterPro; IPR011393; Carotene_ketolase.

DR InterPro; IPR005804; Pa_decat.

DR InterPro; IPR010257; PA_decat_sub.

DR Pfam; PF00487; PA_decatase; 1.

DR PIRSF; PIRSF027840; Carotene_ketolase; 1.

DR Prodom; PD001081; PA_decat_sub; 1.

KW Oxidoreductase.

SO SEQUENCE 329 AA; 37246 MW; 92027CC9AA4252FF CRC64;

Query Match 26.4%; Score 354.5; DB 2; Length 329;

Best Local Similarity 31.5%; Pred. No. 2.3e-23;

Matches 84; Conservative 44; Mismatches 104; Indels 35; Gaps 7;

QY 2 SAHALPKADLTATSLVSGGIIAATLALHYHAL-----DAAAPILA 46

Db 56 NAYKPPSPDTKGITMALR--VIGSWAAVFLHAIFOIKLPTSLDQLHMLPVSDATQALVSG 113

QY 47 VAN-----FLGLTWLVSGLFTIADAMHGSVVPGRPRANAMGQVLVLVYGFGRMK 99

Db 114 TSSLDLIVVFFVLEFLYGLFTTHDAMHGTIALRRQDLNGLVCISLIAMFDYNNML 173

QY 100 IYKMAHHRHAG-TDDDPDFDHGSP--VRVYARFIGTFGRREGLLLPVIVYVALMLGD 156

Db 174 HKRMEHNNHTGVGDPDFRHNPGIVPWFASFMSYSMWQFARLAWTVVMQLLGAP 233

QY 157 RMYTVVFWPLPSILASIQLFVFGIWLPHRP-----GHDAFDRNRNASSRSDPSVSL 209

Db 234 MANLIVFMAAAPILISAFRLFYFGTYVPHKPEPGASGSPAVNMMKSRISQASDLVSFL 293

QY 210 TCFHFGYHHEHLLHPTVPMWRRLPSTR 236

Db 294 TCTHF-DLHMEHHRWPPAPWMLPNCR 319

RESULT 11

06J3NS PRELIMINARY; PRT; 320 AA.

AC 06J3NS; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DB Beta-carotene ketolase.

GN Name=bkt3;

OS Haematococcus pluvialis.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Haematococcaceae; Haematococcus.

OX NCBI_TaxID=44745;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NIES-144;

RA Huang J.-C., Chen F., Sandmann G.;

RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY603347; AY63555.1; -

DR GO; GO:0016701; P:oxidoreductase activity, acting on single d. .; IEA.

DR GO; GO:0016119; P:carotene metabolism; IEA.

DR InterPro; IPR011393; Carotene_ketolase.

DR InterPro; IPR005804; Pa_decat.

DR InterPro; IPR010257; PA_decat_sub.

DR Pfam; PF00487; PA_decatase; 1.

DR PIRSF; PIRSF027840; Carotene_ketolase; 1.

DR Prodom; PD001081; PA_decat_sub; 1.

KW Oxidoreductase.

SO SEQUENCE 320 AA; 35893 MW; 194EE30B2888FCD4 CRC64;

Query Match 26.1%; Score 350.5; DB 2; Length 320;

Best Local Similarity 31.8%; Pred. No. 5.2e-23;

Matches 84; Conservative 39; Mismatches 108; Indels 33; Gaps 7;

QY 3 AARLPKADLTATSLVSGGIIAATLALHYHAL-----W-----FLDAA 40

Db 48 AYKPPSPDTKGITMALR--VIGSWAAVFLHAIFOIKLPTSLDQLHMLPVSEATQALLGS 105

QY 41 AHPILAVANFLGLTWLVSGLFTIADAMHGSVVPGRPRANAMGQVLVLVYGFGRMKI 100

Db 106 SSIHIAAVFIYDEFLYGLFTTHDAMHGTIALRRQDLNGLVCISLIAMFDYSMLH 165

QY 101 IYKMAHHRHAG-TDDDPDFDHGSP--VRVYARFIGTFGRREGLLLPVIVYVALMLGDR 157

Db 166 RKHMEHNNHTGVGDPDFRHNPGIVPWFASFMSYSMWQFARLAWTVVMQLLGAP 225

QY 158 KMYTVVFWPLPSILASIQLFVFGIWLPHRPHGHAFFPRH-----NASSRSDPSVSLTFC 212

Db 226 ANLIVFMAAAPILISAFRLFYFGTYVPHKPEPGASGSPAVNMMKSRISQASDLVSFLTCT 285

QY 213 HFGYHHEHLLHPTVPMWRRLPSTR 236

Db 286 HF-DLHMEHHRWPPAPWMLPNCR 308

RESULT 12

CRTM_HAEPL STANDARD; PRT; 320 AA.

ID CRTM_HAEPL

AC 039982; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 25-OCT-2004 (Rel. 45, Last annotation update)

DB Beta-carotene ketolase (EC 1.13.--) (Beta-carotene oxygenase).

OS Haematococcus pluvialis.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Haematococcaceae; Haematococcus.

OX NCBI_TaxID=44745;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NIES-144;

RX MEDLINE=96046752; PubMed=7579184;

RA Kajiwara S., Kakizono T., Saito T., Kondo K., Ohtani T., Nishio N., Nagai S., Misawa N.;

RT "Isolation and functional identification of a novel cDNA for astaxanthin biosynthesis from Haematococcus pluvialis, and astaxanthin synthesis in *Escherichia coli*.";

RL Plant Mol. Biol. 29:343-352(1995).

CC -1- FUNCTION: Converts beta-carotene to canthaxanthin via echinenone.

CC -1- PATHWAY: Carotenoid biosynthesis. Involved in astaxanthin biosynthetic pathway.

CC -----

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CC or send an email to license@isb-sib.ch).

CC
CC EMBL, D45881; BAA08300.1; -.
CC PIR, S65078; S65078.
CC

DR InterPro; IPR005804; FA_deeat.
DR InterPro; IPR010257; FA_deeat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF027840; Carotene ketolase; 1.
DR Prodom; PD001081; FA_deeat_sub; 1.
DR Carotenoid biosynthesis; Oxidoreductase.
KW

SEQUENCE 320 AA, 35988 MW, 4FAD8669BD326527 CRC64;
SQ

Query Match 25.5%; Score 342.5; DB 1; Length 320;
Best Local Similarity 31.7%; Pred. No. 2.7e-22;
Matches 84; Conservative 39; Mismatches 107; Indels 35; Gaps 8;

QY 3 AAHAPKADLTATSLVSGGIIAAMLAHVHNL-----W-----FLDAA 40
DB 48 AYKPPASDAKGIWALT--IGTWTAVFLHAIPIRLPTSDQLHMLPVSEATQILGGS 105
QY 41 AHPILAVANFLGLTWLSVGLFTIAHDAMGVSVPGRPRANAMGOLVLMYAGFSWRKMI 100
DB 106 SSLHIAAVFLVEFLYGLFTTTDHMGITIALNRQNDLGNICISLYAMFDPYSMH 165
QY 101 VKHMAHHRHAG-TDDDPDFDHGSP--VRWYARFIGTYFGVREGLLPVIVTVYALMLGDR 157
DB 166 RGHWEHNNHTGVBGKDPDFHKGNPGILVPWFASFMSYSLMQFARLAWAVVMQMLGAPM 225
QY 158 WMYVFWPLPSILASIQLFVFGIWLPHRP-----GHDAFDPDRNARSRSISDPVSL 211
DB 226 ANLVFMAAPILVASRLFYFGTYLPHKPEGPAPAGSQVMA-WPRAKTSSEASDVMSFLTC 284
QY 212 FHFGGYHHEHHLHPVWWRLLPSTR 236
DB 285 VHF-DLHWHEHHRWPRAPWQLPHCR 308

RESULT 13

08LJ02 PRELIMINARY; PRT; 276 AA.

AC 08LJ02: 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE BKT.
OS Haematococcus pluvialis.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Haematococcaceae; Haematococcaceae.
OX NCBI_TaxID=44745;
RN [1]
RP SEQUENCE FROM N.A.
RA Teng C.Y., Qin S., Tseng C.K.;
RU Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF534876; FAN03484.1; -.
DR GO; GO:0016701; F:oxidoreductase activity, acting on single d. . .; IEA.
DR GO; GO:0016119; P:carotene metabolism; IEA.
DR InterPro; IPR011393; Carotene ketolase.
DR InterPro; IPR010257; FA_deeat.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF027840; Carotene ketolase; 1.
DR Prodom; PD001081; FA_deeat_sub; 1.
KW Oxidoreductase.
SQ SEQUENCE 276 AA, 30854 MW, 8967DDCC07A0BB90 CRC64;

Query Match 22.4%; Score 300.5; DB 2; Length 276;
Best Local Similarity 30.2%; Pred. No. 1.2e-18;

Matches 81; Conservative 39; Mismatches 95; Indels 53; Gaps 11;

QY 3 AAHAPKADLTATSLVSGGIIAAMLAHVHNL-----W-----FLDAA 40
DB 16 AYKPPASDAKGIWALT--IGTWTAVFLHAIPIRLPTSDQLHMLPVSEATQILGGS 73
QY 41 AHPILAVANFLGLTWLSVGLFTIAHDAMGVSVPGRPRANAMGOLVLMYAGFSWRKMI 100
DB 74 SSLHIAAVFLVEFLYGLFTTTDHMGITIALNRQNDLGNICISLYAMFDPYS--- 130
QY 101 VKHMAHHRHAG-TDDDPDFDHGSP--VRWYARFIGTYFG-VREGLL--LPIVTVYALM 153
DB 131 -MHEHNNHTGVBGKDPDFHKGNPGILVPWFASFMSYSLMQFARLAWAVVMQMLGAPM 189
QY 154 LGDRMYVFWPLPSILASIQLFVFGIWLPHRP-----GHDAFDPDRNARSRSISDPVSL 208
DB 190 AN-----LLVFAAAPILVASRLFYFGTYLPHKPEGPAPAGSQVMSWPRAKTSSEASDVMSF 245
QY 209 LTFHFGGYHHEHHLHPVWWRLLPSTR 236
DB 246 LTCYHFDLF-----APWMOQLPHCR 264

RESULT 14

QYDV2 PRELIMINARY; PRT; 344 AA.

AC QYDV2: 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Beta-carotene hydroxylase (EC 1.14.13.-).
GN Name=crtX; OrderedLocustNames=Pro0266;
OS Prochlorococcus marinus.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1219;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SAG / CCMP 1375 / SS120;
RA MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;
RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Ozlas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weisenbach J., Wincker P.,
RA Wolf Y.I., Hesse W.R.;
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal oxyphototrophic genome."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
DR EMBL; AB017161; AAP9312.1; -.
DR GO; GO:0016701; F:oxidoreductase activity, acting on single d. . .; IEA.
DR GO; GO:0016119; P:carotene metabolism; IEA.
DR InterPro; IPR011393; Carotene ketolase.
DR InterPro; IPR005804; Carotene ketolase.
DR InterPro; IPR010257; FA_deeat_sub.
DR Pfam; PF00487; FA_desaturase; 1.
DR PIRSF; PIRSF027840; Carotene ketolase; 1.
DR Prodom; PD001081; FA_deeat_sub; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 344 AA, 40462 MW, 5D98CAEAF018813A CRC64;

Query Match 14.5%; Score 194.5; DB 2; Length 344;
Best Local Similarity 29.2%; Pred. No. 4.1e-09;
Matches 68; Conservative 38; Mismatches 88; Indels 39; Gaps 15;

QY 20 GIIIAWLAIVHNLFIIDAAHPIAVANFLGLTWLSVGL-FIIADAMGVSVPGRPR 78
DB 46 GGYAIAFLISIW---QWYGVWPLPEVL---VGLAFUSLHMEGTIVHDACHKAHPNK-W 96
QY 79 ANAAGQLVLMYAGFSWRKMI VKMAHHRHAGTDDDPDFH---GSPVWYAR---FI 131
DB 97 INQMGHGA--ILLGFSFPVTRVHLQHSHV-NDPKNDPHIYSTGPPV-WLAPRRFY 153
QY 132 GTYFG-----GILLPIVTVYALMLGDRMYVVF--WPLPSILASIQLFVF 178

Db 154 HEFFFGRLKRLMYELMGMGLERSIPTITVLGVHFNFMNVITNLMFGALMAGVTLGIF 213
 QY 179 GYMLPRPHGDAPDPDHANASSRISDPVSLITCFHFG-GYHHEHHLHPVPPW 230
 Db 214 FYVLPHRP----FMANNKWNKSNRY-PSRYMNLIMGQYHVLVHLMPSIPWP 261

RESULT 15

Q7D5A7 PRELIMINARY; PRT; 672 AA.
 ID Q7D5A7
 AC Q7D5A7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE Pcty acid deesaturase, putative/ferredoxin reductase, electron transfer component.
 GN OrderedlocusNames=MT3658;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxId=1773;
 OX 1)
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RX MEDLINE=22206494; PubMed=12218036;
 RX DOI=10.1128/JB.184.19.5479-5490.2002;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., Deboy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Uterback T.R., Weidman J.F., Khouri H.M., Gill J.C., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
 RA "whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."
 RT J. Bacteriol. 184:5479-5490(2002).
 DR EMBL; AE000516; AAK48018.1; -.
 DR TIGR; MT3658; -.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006058; 2Fe2S fd BS.
 DR InterPro; IPR008333; FAD binding_6.
 DR InterPro; IPR005804; Fd_desat_sub.
 DR InterPro; IPR010257; Fd_desat_sub.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR001709; FPN_cyc_redcse.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00970; FAD binding_6; 1.
 DR Pfam; PF00487; Fd_desaturase; 1.
 DR Pfam; PF00111; Fer2; 1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR PRINTS; PR00371; FPNCR.
 DR PRODOM; PD001081; Fd_desat_sub; 1.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
 KW Iron-sulfur; Metal-binding.
 SQ SEQUENCE 672 AA; 75225 MW; 6E5B476CD1AB57B CRC64;

Query Match 14.2%; Score 190; DB 2; Length 672;

Best Local Similarity 26.4%; Pred. No. 2e-08;

Matches 73; Conservative 38; Mismatches 98; Indels 68; Gaps 16;

QY 5 ALPK-----ADLT-----TSLIVSGGIIAAMLAHVHVMFLDAAHPILAVANFLGLTW 55
 Db 30 ALPTIGIFLATLTAFGSTIAYISGW-IPFWTI-----PVNAAVTFV----- 71
 QY 56 LSVGLFLIADHAGSVVPRPRANAMQQLVLMVAG--FSMRKMIYKMAHHRHAGTD 113
 Db 72 ---MFTVVDASHVAISSIR-WVNGIFGRLA-WLTVGPPVAPAPGYIHIGHRHSND 125
 QY 114 D-DPD--FDHGG--PVRW-YARFIGYFGMREGILLPVIVT-----VVA 151
 Db 126 EDDPDVFAHSGSLMWVPLRWSWVEFYIKYLLPRGRSPVIEVAETLVMMTLPLTGLIVA 185

QY 152 LMLGRRMYVFWPPLPSILASIQLFVPGIMLPHRPGHDA-FPDRHNAASSRIS-----DP 205
 Db 186 IYTGMPWTLAIYFLIPQRIGLTVLAWMPWMLPHHGLEDTQRGRNRYRATNRRYGAEWLP 245
 QY 206 VSLITCFHFGGYHHEHHLHPVPMWRLPSTRTKGDTA 242
 Db 246 VLSQ-----NYHLVHLLPSPVFFRYLRTWRNEEA 277

Search completed: June 17, 2005, 19:37:06
 Job time : 94.1378 secs

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CC The invention relates to an isolated polypeptide having the activity of
CC an enzyme such as hydroxymethylglutaryl Coenzyme-A (HMGCoA) reductase,
CC isopentenyl diphosphate isomerase, HMGCoA synthase, mevalonate kinase,
CC phosphomevalonate kinase or diphosphomevalonate decarboxylase. The
CC invention also relates to the production of a carotenoid-producing cell
CC and engineering a bacterium to produce an isoprenoid compound, comprising
CC culturing a parent bacterium in a medium permitting expression of an
CC isoprenoid compound and selecting a mutant bacterium from the culture
CC medium that produces 1.1-1000 times more isoprenoid compound than the
CC parent bacterium, introducing an expression vector comprising a *farnesyl*
CC diphosphate (FPP) synthase DNA fragment operably linked to an expression
CC control sequence into the mutant bacterium, and selecting a bacterium
CC that contains the expression vector and produces at least 1.1 times more
CC isoprenoid compound than the selected mutant. The cell is useful for
CC producing a carotenoid (phycoene, lycopene, beta-carotene, zeaxanthin,
CC canthaxanthin, astaxanthin, adonixanthin, cryptoxanthin, echinenone or
CC adonirubin) by culturing the cell under conditions permitting expression
CC of the polypeptide encoded by the polynucleotide sequence and isolating
CC the carotenoid from the cell or the medium of the cell. The carotenoids
CC (C-4- isoprenoid compounds) are used as nutritional supplements,
CC pharmaceuticals, food colourants and pigments for animal feeds. This
CC sequence represents DNA encoding a polypeptide of the invention
XX
XX
SQ Sequence 729 BP; 100 A; 244 C; 232 G; 153 T; 0 U; 0 Other;

Query Match 100.0%; Score 729; DB 8; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.6e-153;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGCATGCTCCCTGCGCCCAAGCGATGTCGACCGCCACCAAGTTTGTCTCGGCG 60
DB 1 ATGAGCGCATGCTCCCTGCGCCCAAGCGATGTCGACCGCCACCAAGTTTGTCTCGGCG 60
QY 61 GGCATCATCGCCGCGTGGCGCCCTGCGATGTCGATGCGCTGCTTGTGACCGCGCG 120
DB 61 GGCATCATCGCCGCGTGGCGCCCTGCGATGTCGATGCGCTGCTTGTGACCGCGCG 120
QY 121 GGCATCCCATCTGCGCGTGGCGATTTCTCGGGCTGACCTGCGTGTCTCGGCTG 180
DB 121 GGCATCCCATCTGCGCGTGGCGATTTCTCGGGCTGACCTGCGTGTCTCGGCTG 180
QY 181 TTCATCATGCGCGATGACGCGATGTCGATGCGTGTCTGCGCGCGCGCGCGCAT 240
DB 181 TTCATCATGCGCGATGACGCGATGTCGATGCGTGTCTGCGCGCGCGCGCGCAT 240
QY 241 GGGGCGATGGCGAGCTTGTCTGCGTGTGTCGCGATTTCTCGGGCGCAAGATGATC 300
DB 241 GGGGCGATGGCGAGCTTGTCTGCGTGTGTCGCGATTTCTCGGGCGCAAGATGATC 300
QY 301 GTCAGACATGGCCCATCATGCGCATGCGGAAACGACGACCCCAATTTTCAGCAT 360
DB 301 GTCAGACATGGCCCATCATGCGCATGCGGAAACGACGACCCCAATTTTCAGCAT 360
QY 361 GCGCGCGCGGCTGCGTGTGTCGCGCTTTCATGCGGACCTATTTTGGCTGCGCGAG 420
DB 361 GCGCGCGCGGCTGCGTGTGTCGCGCTTTCATGCGGACCTATTTTGGCTGCGCGAG 420
QY 421 CTGCGTGTGCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTC 480
DB 421 CTGCGTGTGCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTC 480
QY 481 GTGCTCTTGTGCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTC 540
DB 481 GTGCTCTTGTGCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTC 540
QY 541 TGGCTGCGCGACCGCGCGCGCGCGACGAGCGGTTCCGCGACCGCAAGTCGCGGTCG 600
DB 541 TGGCTGCGCGACCGCGCGCGCGCGACGAGCGGTTCCGCGACCGCAAGTCGCGGTCG 600
QY 601 CGGATCAGGACCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTC 660
DB 601 CGGATCAGGACCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTCGCGTGTGTC 660

QY 661 CACCACTGACACCGGAGTGTCTTGTGCGCTTGTGCGCGCTGCGACACCGCGACCAAGGGGAC 720
DB 661 CACCACTGACACCGGAGTGTCTTGTGCGCTTGTGCGCGCTGCGACACCGCGACCAAGGGGAC 720
QY 721 ACCGATGCA 729
DB 721 ACCGATGCA 729

RESULT 2

AAV40170
ID AAV40170 standard; DNA, 1261 BP.

AAV40170;
AC

10-AUG-1999 (first entry)
DT

DNA sequence in Fig 59-60 of JP10155497.
DE

Carotenoid; pigment; canthaxanthin; R1534; *crb*; prephyloene synthase;
KW *crf*; phycoene desaturase; *crf*; lycopene cyclase; *crf*2396;
KW beta-carotene beta-oxygenase; food product; fermentation; *ds*.

Flavobacterium sp.
OS

JP10155497-A.
PN

16-JUN-1998.
PD

02-DEC-1997; 97JP-00348653.
PF

02-DEC-1996; 96EP-00810839.
PR

(HOFF) HOFFMANN LA ROCHE & CO AG F.
PA

WPI, 1998-391048/34.
DR

Preparation of carotenoid - comprises fermentation with transformed cell.
PT

Example 8; Fig 59-60; 80pp; Japanese.
PS

The invention describes the preparation of carotenoid pigments e.g.
CC canthaxanthin using a cell transformed by a vector having DNA sequences
CC (a) to (e) or substantially homologous sequences. (a) a DNA sequence
CC (*crf*) coding GGP synthase of Flavobacterium sp. R1534; (b) a DNA
CC sequence (*crb*) coding prephycoene synthase of Flavobacterium sp. R1534;
CC (c) a DNA sequence (*crf*) coding phycoene desaturase of Flavobacterium
CC sp. R1534; (d) a DNA sequence (*crf*) coding lycopene cyclase of
CC Flavobacterium sp. R1534, and (e) a DNA sequence (*crf*2396) coding beta-
CC carotene beta-oxygenase of a microbe E-396 (FERM BP-4283). The carotenoid
CC or a carotenoid mixture can also be used in preparation of food products.
CC The method is an improved method of fermentation for carotenoid
CC production
XX

SQ Sequence 1261 BP; 188 A; 411 C; 406 G; 256 T; 0 U; 0 Other;

Query Match 100.0%; Score 729; DB 2; Length 1261;
Best Local Similarity 100.0%; Pred. No. 1.8e-153;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGCATGCTCCCTGCGCCCAAGCGATGTCGACCGCCACCAAGTTTGTCTCGGCG 60
DB 40 ATGAGCGCATGCTCCCTGCGCCCAAGCGATGTCGACCGCCACCAAGTTTGTCTCGGCG 99
QY 61 GGCATCATCGCCGCGTGGCGCCCTGCGATGTCGATGCGCTGCTTGTGACCGCGCG 120
DB 100 GGCATCATCGCCGCGTGGCGCCCTGCGATGTCGATGCGCTGCTTGTGACCGCGCG 159
QY 121 GGCATCCCATCTGCGCGTGGCGATTTCTCGGGCTGACCTGCGTGTCTGCGTGTGTC 180
DB 160 GGCATCCCATCTGCGCGTGGCGATTTCTCGGGCTGACCTGCGTGTCTGCGTGTGTC 219
QY 181 TTCATCATGCGCGATGACGCGATGTCGATGCGTGTCTGCGCGCGCGCGCGCAT 240


```

Db      220 TTTCATATGCGCATGACCGGATGATGAGTGGTGGTGGCGGGGGCCCGCCGCAAT 279
Qy      241 GCGGCGATGGGCGACGCTTGTCTGTGTATGATGCGGATTTTCTGGCGCAAGATGATC 300
Db      280 GCGGCGATGGGCGACGCTTGTCTGTGTATGATGCGGATTTTCTGGCGCAAGATGATC 339
Qy      301 GTCAAGACATGGGCGATGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 360
Db      340 GTCAAGACATGGGCGATGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 399
Qy      361 GCGGCGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 420
Db      400 GCGGCGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 459
Qy      421 CTGCTGCTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 480
Db      460 CTGCTGCTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 519
Qy      481 GTGCTGCTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 540
Db      520 GTGCTGCTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 579
Qy      541 TGCGTCCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db      580 TGCGTCCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 639
Qy      601 CGGATCAGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db      640 CGGATCAGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 699
Qy      661 CACCACTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db      700 CACCACTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 759
Qy      721 ACCGATGA 729
Db      760 ACCGATGA 768

RESULT 3
AAV40147
ID      AAV40147 standard; DNA; 729 BP.
XX      AAV40147;
XX      10-AUG-1999 (first entry)
DE      DNA sequence (crtW2396) encoding a beta-carotene beta-oxygenase.
XX      Carotenoid; pigment; canthaxanthin; R1534; crtB; prephytylene synthase;
XX      crtI; phytylene desaturase; crtY; lycopene cyclase; crtW2396;
XX      beta-carotene beta-oxygenase; food product; fermentation; ds.
OS      Flavobacterium sp.
XX      JP10155497-A.
XX      16-JUN-1998.
XX      02-DEC-1997; 97JP-00348653.
XX      02-DEC-1996; 96EP-00810839.
XX      (HOPF) HOPFMANN LA ROCHE & CO AG F.
XX      WPI; 1998-391048/34.
XX      P-RSDB; AAM69535.
XX      Preparation of carotenoid - comprises fermentation with transformed cell.
XX      Claim 1; Fig 61; 80pp; Japanese.

```

CC The invention describes the preparation of carotenoid pigments e.g. CC canthaxanthins using a cell transformed by a vector having DNA sequences CC (a) to (e) or substantially homologous sequences. (a) a DNA sequence CC (crtE) coding GPP synthase of Flavobacterium sp. R1534; (b) a DNA sequence CC (crtB) coding prephytylene synthase of Flavobacterium sp. R1534; CC (c) a DNA sequence (crtI) coding phytylene desaturase of Flavobacterium CC sp. R1534; (d) a DNA sequence (crtY) coding lycopene cyclase of CC Flavobacterium sp. R1534; and (e) a DNA sequence (crtW2396) coding beta- CC carotene beta-oxygenase of a microbe B-396 (FERM BP-4283). The carotenoid CC or a carotenoid mixture can also be used in preparation of food products. CC The method is an improved method of fermentation for carotenoid CC production

XX SQ Sequence 729 BP; 100 A; 245 C; 231 G; 153 T; 0 U; 0 Other;

Query Match 99.8%; Score 727.4; DB 2; Length 729;

Best Local Similarity 99.9%; Pred. No. 3.7e-153;

Matches 728; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1 ATGAGCGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Db      1 ATGAGCGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Qy      61 GCGATCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db      61 GCGATCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Qy      121 GCGATCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db      121 GCGATCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Qy      181 TTTCATATGCGCGATGACGCGATGACGCGATGACGCGATGACGCGATGACGCGATGACGCGAT 240
Db      181 TTTCATATGCGCGATGACGCGATGACGCGATGACGCGATGACGCGATGACGCGATGACGCGAT 240
Qy      241 GCGGCGATGGGCGACGCTTGTCTGTGTATGATGCGGATTTTCTGGCGCAAGATGATC 300
Db      241 GCGGCGATGGGCGACGCTTGTCTGTGTATGATGCGGATTTTCTGGCGCAAGATGATC 300
Qy      301 GTCAAGACATGGGCGATGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 360
Db      301 GTCAAGACATGGGCGATGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 360
Qy      361 GCGGCGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 420
Db      361 GCGGCGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 420
Qy      421 CTGCTGCTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 480
Db      421 CTGCTGCTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 480
Qy      481 GTGCTGCTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 540
Db      481 GTGCTGCTGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 540
Qy      541 TGCGTCCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db      541 TGCGTCCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Qy      601 CGGATCAGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db      601 CGGATCAGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Qy      661 CACCACTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db      661 CACCACTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Qy      721 ACCGATGA 729
Db      721 ACCGATGA 729

```

RESULT 4

ID	AD061160 standard; DNA; 729 BP.
AC	AD061160;
DJ	15-JUL-2004 (first entry)
DE	P. marcusii ketolase DNA.
KW	d8; Ketocarotenoid; plant; ketolase; petal; flower-specific promoter; petal-specific promoter; epsilon-cyclase; ec; chromoplast; hydroxylase; beta-glycase; bc; astaxanthin; canthaxanthin; echinenone; adonitrubin; adonixanthin; ornamental; food; animal feed; supplement; pigment; colouring; trout; salmon; shrimp; gene.
OS	Paracoccus marcusii.
FH	Key Location/Qualifiers
FT	CDS 1..729
FT	/tag= a
FT	/product= "ketolase"
FN	DEI0238978-A1.
PD	04-MAR-2004.
PF	20-AUG-2002; 2002DE-01038978.
PR	20-AUG-2002; 2002DE-01038978.
PA	(SUNG-) SUNGENE GMBH & CO KGAA. WPI; 2004-215840/21. P-PADB; AD061161.
PT	Method for preparing ketocarotenoids, useful e.g. as food or feed supplements, by increasing, or introducing, ketolase activity in the fruits of transgenic plants, also new nucleic acid constructs.
XX	Disclosure; SEQ ID NO 9; 77bp; German.
XX	This invention describes a novel method for preparing ketocarotenoids by culturing genetically modified plants that, in comparison with the wild-type, have altered ketolase activity in the fruits. The invention also describes a nucleic acid construct comprising a fruit-specific promoter linked functionally to a sequence that encodes the altered ketolase, genetically modified plants in which the fruits have altered ketolase activity and method for preparing such plants. The plants contain at least one nucleic acid sequence that encodes the ketolase, especially under control of a fruit-specific promoter, and particularly they contain chromoplasts in the fruit. The ketolase-encoding nucleic acid is inserted by standard methods, then the transgenic plants are cultivated, harvested and ketocarotenoids are isolated from their fruits. Preferred carotenoid include astaxanthin, cantaxanthin, echinenone (or its 3'- or 3''-hydroxy derivatives) adonitrubn or adonixanthin. The modified plants with increased ketolase activity are used as ornaments/as food or animal feed and for preparation of ketocarotenoids-containing extracts or for preparing food/feed supplements, e.g., especially where the ketocarotenoid is astaxanthin, as a pigment for colouring trout, salmon and shrimps. The transgenic plants produce fruits with increased content of ketocarotenoids. The invention describes a construct, vector pSKETO2 which comprises, in pSN5, a cassette containing the constitutive double 35S cauliflower mosaic virus promoter; the rbcS chloroplast transit peptide; the ketolase gene from Haemoccus pluvialis and a terminator. It was used to transform tomato cells, using Agrobacterium tumefaciens, and the infected cells regenerated to plants conventionally. One of the resulting transgenic lines, CS13-24, produced fruits that contained lycopene, beta-carotene, cantaxanthin, adonitrubn or astaxanthin, but the last three were absent from wild-type fruits (which additionally contained lutein, not detected in transgenic fruits).
SEQ	Sequence 729 BP; 103 A; 24 C; 231 G; 151 T; 0 U; 0 Other;

Query Match	95.8%;	Score 698.6;	DB 12;	Length 729;
Best Local Similarity	97.4%;	Pred. No. 1e-146;		
Matches 710;	Conservative 0;	Mismatches 19;	Indels 0;	Gaps 0
QY	1	ATGAGCGCACAATGCGCCCTGCGCCCAAGGACAGATCTGACCCGGCACCAAGTTTGATCGTCTCGAGC	60	
Db	1	ATGAGCGCACAATGCGCCCTGCGCCCAAGGACAGATCTGACCCGGCACCAAGCTTATCTCTCGGGC	60	
QY	61	GGCATCATCGCGCGGTGAGTGGCCCTGCGATGTGCAATGCGCTGTGTCTTCTGACCGGCG	120	
Db	61	GGCATCATCGCGCGATGAGTGGCCCTGCGATGTGCAATGCGCTGTGTCTTCTGACCGGCG	120	
QY	121	GGCGATCCCATCTCGGCGGTGCGGCAATTTCTCTGGGAGCTGACCTGGCTGTCCGTCTGG	180	
Db	121	GCCCATCCCATCTCGGCGGTGCGGCAATTTCTCTGGGAGCTGACCTGGCTGTCCGTCTGGATTT	180	
QY	181	TTTCATCATCGGCGCATGACGGATGATGGGTCCGGTCGCGCGGGCGCCCGCGCGCAT	240	
Db	181	TTTCATCATCGGCGCATGACGGATGACGGGTCCGGTCGCGCGGGCGTCGCCGCCCAT	240	
QY	241	GGCGCGATGGGCGCAGCTGTCTCTGTGGCTGTATGCGGATTTTCTCGGCGCAAGATGATC	300	
Db	241	GGCGCGATGGGCGCAGCTGTCTCTGTGGCTGTATGCGGATTTTCTCGGCGCAAGATGATC	300	
QY	301	GTCAAGCACAATGGCCCATCATCGCCATGCCGAAACCGACGACGACCCAGATTTTGCACCAT	360	
Db	301	GTCAAGCACAATGGCCCATCATCGCCATGCCGAAACCGACGACGACCCAGATTTTGCACCAT	360	
QY	361	GGCGCGCCGGTCCGCTGGTACGCCCGGCTTCAATCGGCACTTATTTTCGGCTGGCGGAGGGG	420	
Db	361	GGCGCGCCGGTCCGCTGGTACGCCCGGCTTCAATCGGCACTTATTTTCGGCTGGCGGAGGGG	420	
QY	421	CTGCTGCTGCGCCGTCATCGTACCGGTCTATGCGCTGATGTGGGGATTCGCTGATGTAC	480	
Db	421	CTGCTGCTGCGCCGTCATCGTACCGGTCTATGCGCTGATTCCTGGGGATTCGCTGATGTAC	480	
QY	481	GTGGTCTTTCTGAGCGGTGCGTGCATCTTGAGGTGCATCCAGCTGTTGCTGTTCCGCGATC	540	
Db	481	GTGGTCTTTCTGAGCGGTGCGTGCATCTTGAGGTGCATCCAGCTGTTGCTGTTCCGCGACT	540	
QY	541	TGGCTGCGCGCACCGGCCCGGCGACAGACCGGTTCCCGGACCGCCCAATAGCGCGTCCGTCG	600	
Db	541	TGGCTGCGCGCACCGGCCCGGCGACAGACCGGTTCCCGGACCGCCCAATAGCGCGTCCGTCG	600	
QY	601	CGGATTCAGCGACCCCGGTGCGCTGTGACCTGCTTTTCACTTTTGGCGGTTATCATACGAA	660	
Db	601	CGGATTCAGCGACCCCTGTGTCCGTCTGACCTGCTTTTCACTTTTGGCGGTTATCATACGAA	660	
QY	661	CACCAACCTGACCCCGACCGGTGCTTGTGTGGCGGCTGCCACAGACCCGACCAAGGGGGAGC	720	
Db	661	CACCAACCTGACCCCGACCGGTGCTTGTGTGGCGGCTGCCACAGACCCGACCAAGGGGGAGC	720	
QY	721	ACCGCATGA 729		
Db	721	ACCGCATGA 729		
RESULT 5				
ADO61077				
ID	ADO61077	standard; DNA; 729 BP.		
XX	ADO61077;			
XX	15-JUN-2004	(first entry)		
XX	P. marcusii	ketolase DNA.		
XX	ds:	ketocarotenoid; plant; ketolase; petal; flower-specific promoter;		
XX	petal-specific promoter; epsilon-cyclase; c;	chromoplast; hydroxylase;		
XX	beta-cyclase; bc; beta-xanthin; canthaxanthin; echinenone; adonirubin;			
XX	adonirubin; ornamental; food; animal feed; supplement; pigment;			
XX	colouring; trout; salmon; shrimp;			

OS Paracoccus marcusii.
 XX Key Location/Qualifiers
 FH CDS 1..729
 FT /tag= a
 XX
 XX DE10238980-A1.
 XX
 XX 04-MAR-2004.
 XX
 XX 20-AUG-2002; 2002DE-01038980.
 XX
 XX 20-AUG-2002; 2002DE-01038980.
 XX
 XX (SUNG-) SUNGENE GMBH & CO KGAA.
 XX
 XX WPI; 2004-215842/21.
 XX P-PSDB; ADO61078.
 XX
 XX Method for preparing ketocarotenoids, useful e.g. as food or feed
 PT supplements, by increasing, or introducing, ketolase activity in the
 PT petals of transgenic plants, also new nucleic acid constructs.
 PT
 XX Disclosure; SEQ ID NO 9; 140pp; German.
 XX
 XX This invention describes a novel method for preparing ketocarotenoids by
 CC culturing genetically modified plants that, in comparison with the wild-
 CC type, have altered ketolase activity in the petals. The invention also
 CC describes a nucleic acid construct containing a nucleic acid that encodes
 CC ketolase, linked functionally to a flower- or petal-specific promoter,
 CC double-stranded RNA that comprises a sense strand, including a sequence
 CC that is essentially identical with at least part of the RNA epsilon-
 CC cyclase (ec) transcript or the promoter region of the ec gene and an
 CC antisense strand that is essentially complementary to the sense strand,
 CC a transgenic expression cassette comprising a plant-functional promoter
 CC linked to a nucleic acid that transcribes double-stranded RNA,
 CC genetically altered plant in which activity of ketolase in the petals is
 CC increased, if already present in the wild-type or introduced if absent
 CC from the wild type, genetically altered plant that has chromoplasts in
 CC the petals and contains at least one transgenic nucleic acid that encodes
 CC a ketolase. Particularly plants also have increased activity, relative to
 CC wild type, of hydroxylase and/or beta-cyclase (bc) activity, especially
 CC as a result of introducing the appropriate nucleic acid, and plants are
 CC also selected for highest activity of these two enzymes. The transgenic
 CC plants are cultivated, harvested and ketocarotenoids isolated from their
 CC petals. Preferred carotenoids include astaxanthin, canthaxanthin,
 CC echinone (or its 3- or 3'-hydroxy derivatives), adonixanthin or
 CC adonixanthin. The modified plants with increased ketolase activity are
 CC used as ornamentals, as food or animal feed and for preparation of
 CC ketocarotenoid-containing extracts or for preparing food/feed
 CC supplements, e.g., especially where the ketocarotenoid is astaxanthin, as
 CC a pigment for colouring trout, salmon and shrimps. The transgenic plants
 CC have increased content of ketocarotenoids. Vector p53KXTO2 comprises, in
 CC PSUN5, a cassette containing the constitutive double 35S cauliflower
 CC mosaic virus promoter, the rbcS chloroplast transit peptide, the ketolase
 CC gene from Haemophilus pluvialis and a terminator. The vector was used to
 CC transform tomato cells, using Agrobacterium tumefaciens and the infected
 CC cells regenerated to plants conventionally. One of the resulting
 CC transgenic lines, CS13-8, produced orange flowers (yellow in the wild
 CC type) and its petals contained astaxanthin and adonixanthin, both absent
 CC from the wild type.
 XX
 XX Sequence 729 BP; 103 A; 244 C; 231 G; 151 T; 0 U; 0 Other;
 SQ
 Query Match 95.8%; Score 698.6; DB 12; Length 729;
 Best Local Similarity 97.4%; Pred. No. 1e-146;
 Matches 710; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 ATGAGGCGACATGCTCCGCGCAAGGACATGACCGCCACCACTTTGATGCTGCGGC 60
 DB 1 ATGAGGCGACATGCTCCGCGCAAGGACATGACCGCCACCACTTTGATGCTGCGGC 60
 QY 61 GGATCATGCGCGCGTGGCGCTGACATGTGATGCGGTGTGTTTGGACGCGGCG 120

DB 61 GGATCATGCGCGCGTGGCGCTGACATGTGATGCGGTGTGTTTGGACGCGGCG 120
 QY 121 GCGATCCCATCTTGGCGGTGCGGAATTTCTCGGGCTGACCTTGCTGCTGGTCTG 180
 DB 121 GCGATCCCATCTTGGCGGTGCGGAATTTCTCGGGCTGACCTTGCTGCTGGTCTG 180
 QY 181 TTCATCATGCGCATGAGCGGATGAGATGAGGTGCTGTCGCGGGGCGCGCGCAAT 240
 DB 181 TTCATCATGCGCATGAGCGGATGAGATGAGGTGCTGTCGCGGGGCGCGCGCAAT 240
 QY 241 GCGCGATGCGCGCAGCTTGTCTGTGCTGTATGCGGATTTTCTCGGCGCAATGATC 300
 DB 241 GCGCGATGCGCGCAGCTTGTCTGTGCTGTATGCGGATTTTCTCGGCGCAATGATC 300
 QY 301 GTCAAGCACATGCGCCCATATGATGCGGACCGGAAACCGACGACATTTTCACCAT 360
 DB 301 GTCAAGCACATGCGCCCATATGATGCGGACCGGAAACCGACGACATTTTCACCAT 360
 QY 361 GCGGCGCGCGGTGCGGTGAGCGCGGCTTATGCGGACCTATTTGCGGTGCGCGAGG 420
 DB 361 GCGGCGCGCGGTGCGGTGAGCGCGGCTTATGCGGACCTATTTGCGGTGCGCGAGG 420
 QY 421 CTGCTGCTGCGCGGTATGCTGACCGGTCTATGCGCTGATGTTGGGGATGCTGATGAC 480
 DB 421 CTGCTGCTGCGCGGTATGCTGACCGGTCTATGCGCTGATGTTGGGGATGCTGATGAC 480
 QY 481 GTGCTTTTGTGCGCTGCTGCTGATCTTGCGGTGATGCTGCTGCTGCTGCTGCTG 540
 DB 481 GTGCTTTTGTGCGCTGCTGCTGATCTTGCGGTGATGCTGCTGCTGCTGCTGCTG 540
 QY 541 TGGCTGCGCGACCG 600
 DB 541 TGGCTGCGCGACCG 600
 QY 601 CGATCAGCGACCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 601 CGATCAGCGACCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 661 CACCATCTGACCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 DB 661 CACCATCTGACCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 721 ACCGATGA 729
 DB 721 ACCGATGA 729
 RESULT 6
 ID AD038246
 ID AD038246 standard; DNA; 729 BP.
 AC AD038246;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 XX Paracoccus marcusii ketolase DNA.
 XX
 XX astaxanthin; plant; animal feed; fodder; fish; crustacean; bird;
 KW salmonid; shrimp; crab; hen; duck; geese; flamingo; ketolase;
 KW beta-carotene; canthaxanthin; hydroxylase; beta-cyclase; pigmentation;
 KW trout; salmon; shrimp; ds; gene.
 XX
 XX Paracoccus marcusii.
 OS
 XX Key Location/Qualifiers
 FH CDS 1..729
 FT /tag= a
 FT /product= "ketolase"
 XX
 XX DE10258971-A1.
 XX
 XX 01-JUL-2004.

XX 16-DEC-2002; 2002DE-01058971.
 PF 16-DEC-2002; 2002DE-01058971.
 PR (SUNG-) SUNGENE GMBH & CO KGAA.
 XX
 PA WPI; 2004-554601/54.
 XX P-PSDB; ADQ38247.
 DR
 XX
 PT Use of astaxanthin-containing plant material, or extracts, from Tagetes
 PT for oral administration to animals, particularly for pigmentation of
 PT fish, crustacea, birds and their products.
 PS
 XX Disclosure; SEQ ID NO 9; 145bp; German.

CC This invention describes the novel use of astaxanthin-containing plants
 CC (particularly the flower heads or petals) of the genus Tagetes or their
 CC parts for oral administration to animals. Methods are also described for
 CC a) the preparation of an animal feed composition by mixing standard
 CC fodder ingredients with astaxanthin-containing plants, b) for
 CC pigmentation of animals, or their products, by oral administration of
 CC astaxanthin-containing plants and c) animal feed composition or
 CC pigmentation agent that contains astaxanthin-containing plants. The
 CC plants, or their parts or extracts, are administered directly to animals,
 CC optionally after intermediate processing, or they are formulated with
 CC fodder components. Particularly they are administered to fish,
 CC crustaceans or birds, specifically salmonids, shrimps, crabs, hens,
 CC ducks, geese and flamingoes. The plants of the invention are preferably
 CC modified to provide ketolase activity, for conversion of beta-carotene to
 CC canthaxanthin, particularly with the highest level of expression in the
 CC flowers, e.g. by using a flower-specific promoter. The plants may also
 CC have increased activity of hydroxylase (for conversion of canthaxanthin
 CC to astaxanthin) and/or of beta-cyclase (to increase production of beta-
 CC carotene from gamma-carotene). Astaxanthin-containing compositions are
 CC used particularly for pigmentation of animals, preferably fish, crustacea
 CC and birds, or their products (meat, skin, feathers and eggs), most
 CC particularly trout, salmon and shrimp. Genetically modified Tagetes
 CC produce larger amounts of astaxanthin than the current source, Adonis
 CC aestivalis, and more cheaply. The invention uses expression vector
 CC pSKR02 which includes a cassette consisting of the double 35S promoter,
 CC the sequence for the pea rbc transit peptide, the sequence encoding a
 CC ketolase (beta-carotene-4-oxygenase) from Haemotococcus pluvialis and the
 CC polyadenylation signal from cauliflower mosaic virus. It was used to
 CC transform leaves of Tagetes, by Agrobacterium-mediated transfer, then
 CC these regenerated to plants.

XX Sequence 729 BP; 103 A; 244 C; 231 G; 151 T; 0 U; 0 Other;

XX Query Match 95.8%; Score 698.6; DB 12; Length 729;

XX Best Local Similarity 97.4%; Pred. No. 1e-146; Matches 710; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 ATGAGCGCATGCTGCTCCCAAGGAGATCTGACCGCCACCAAGTTTGTCTCGGGC 60
 DB 1 ATGAGCGCATGCTGCTCCCAAGGAGATCTGACCGCCACCAAGTTTGTCTCGGGC 60
 QY 61 GGCATCATGCGCGCGTGGCGCTGCGATGTCGATGCGGCTTCTGACGCGCGG 120
 DB 61 GGCATCATGCGCGCGTGGCGCTGCGATGTCGATGCGGCTTCTGACGCGCGG 120
 QY 121 GGCATCATGCGCGCGTGGCGATTTCTGCGGCTGACCTGAGCTGCGTGGTCTG 180
 DB 121 GGCATCATGCGCGCGTGGCGATTTCTGCGGCTGACCTGAGCTGCGTGGTCTG 180
 QY 181 TTTCATCATGCGCGATGACGCGATGTCGTCGTCGTCGCGCGCGCGCAAT 240
 DB 181 TTTCATCATGCGCGATGACGCGATGTCGTCGTCGTCGCGCGCGCGCAAT 240
 QY 241 GCGGCGATGCGCGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 300
 DB 241 GCGGCGATGCGCGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 300

QY 301 GTCAAGCATATGCTCCATCATGCGCCAGAACCGACGACGACCCAGATTTGACCAT 360
 DB 301 GTCAAGCATATGCTCCATCATGCGCCAGAACCGACGACGACCCAGATTTGACCAT 360
 QY 361 GCGGCGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 420
 DB 361 GCGGCGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 420
 QY 421 CTGCTGCTGCGCGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 480
 DB 421 CTGCTGCTGCGCGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 480
 QY 481 GTGCTCTTGTGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 540
 DB 481 GTGCTCTTGTGCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 540
 QY 541 TGGCTGCGCGACCG 600
 DB 541 TGGCTGCGCGACCG 600
 QY 601 CGGATCAGCGACCG 660
 DB 601 CGGATCAGCGACCG 660
 QY 661 CACCACTGACACCG 720
 DB 661 CACCACTGACACCG 720
 QY 721 ACCGATGTA 729
 DB 721 ACCGATGTA 729

RESULT 7

ID ADR03861 standard; DNA; 729 BP.

AC ADR03861;

DT 21-OCT-2004 (first entry)

DE Paracoccus marcusii ketolase coding sequence SEQ ID NO: 19.

XX carotenoid; genetically modified; Blakeslea; nutrient; pigmentation;

KW antioxidant; transgenic; ds; gene; ketolase; enzyme.

XX Paracoccus marcusii.

OS Synthetic.

FT Key Location/Qualifiers

FT CDS 1..729

FT /tag= a

FT /product= "ketolase"

XX WO2004063359-A2.

XX 29-JUL-2004.

XX 09-JAN-2004; 2004WO-EP000099.

XX 09-JAN-2003; 2003DE-01000649.

XX 08-SEP-2003; 2003DE-01041271.

XX (BADI) BASF AG.

XX Matuschek M, Klein D, Heinekamp T, Schmidt A, Brakhage A;

XX Achatz B;

XX WPI; 2004-544088/52.

XX P-PSDB; ADR03862.

PT Preparing carotenoids or their precursors useful e.g. in cosmetics,

PT pharmaceuticals, foods and animal feeds, comprises culturing genetically

PT modified Blakeslea.

XX Disclosure; SEQ ID NO 19; 486pp; German.

CC The present invention relates to a method of preparing carotenoids or
CC their precursors using genetically modified organisms of the genus
CC Blakeslea. The method is used for production of carotenoids, particularly
CC carotenes and xanthophylls, useful as animal and human nutrients, or
CC supplements, cosmetics, dermatological agents and pharmaceuticals,
CC particularly for pigmentation or colouring beverages, but also as
CC antioxidants. The present sequence is a polynucleotide used in the
CC exemplification of the invention.

XX Sequence 729 BP; 103 A; 244 C; 231 G; 151 T; 0 U; 0 Other;

Query Match 95.8%; Score 698.6; DB 13; Length 729;

Best Local Similarity 97.4%; Pred. No. 1e-146; Mismatches 19; Indels 0; Gaps 0;

Matches 710; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

1 ATGAGGCGACATGCGCTGCGCCCAAGGAGATCTGACCGCCACCGATTGATCGTGGGGC 60
1.ATGAGGCGACATGCGCTGCGCCCAAGGAGATCTGACCGCCACCGATTGATCGTGGGGC 60
61 GGCATCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 120
61 GGCATCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 120
61 GGCATCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 120
121 GGCATCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 180
121 GGCATCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 180
121 GGCATCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 180
181 TTCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 240
181 TTCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 240
241 GCGCGCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 300
241 GCGCGCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 300
241 GCGCGCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 300
301 GTCACGACATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 360
301 GTCACGACATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 360
361 GCGCGCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 420
361 GCGCGCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 420
361 GCGCGCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 420
421 GCGCGCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 480
421 GCGCGCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 480
421 GCGCGCATGCGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 480
481 GTCGCTGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 540
481 GTCGCTGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 540
481 GTCGCTGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 540
541 TGGCTGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 600
541 TGGCTGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 600
541 TGGCTGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 600
601 CGGATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 660
601 CGGATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 660
601 CGGATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 660
661 CACCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 720
661 CACCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 720
661 CACCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 720
721 ACCGATGTA 729
721 ACCGATGTA 729

RESULT 8

ADRO3941

ID ADRO3941 standard; DNA; 729 BP.

XX ADRO3941;

AC 21-OCT-2004 (first entry)

XX P marcusii ketolase coding sequence.

XX gene; genetically modified; vector; carotenoid production; pigmentation;

XX nutrient; antioxidant; ds; ketolase; enzyme.

XX Paracoccus marcusii.

OS Synthetic.

FT Key Location/Qualifiers

FT CDS 1..729

FT /tag= a

FT /product= "ketolase"

PN MO2004063358-A1.

XX 29-JUL-2004.

XX 09-JAN-2004; 2004WO-BP000100.

XX 09-JAN-2003; 2003DE-01000649.

XX 08-SEP-2003; 2003DE-01041272.

XX (BADI) BASF AG.

XX Matuschek M, Heinkeamp T, Schmidt A, Brakhage A;

XX WPI; 2004-544087/52.

XX P-PSDB; ADRO3942.

XX Preparing genetically modified Blakeslea, useful for preparation of

XX carotenoids, useful as food additives, cosmetics or pharmaceuticals,

XX comprises transformation, optional homokaryotizing, and selection.

XX Disclosure; SEQ ID NO 19; 459pp; German.

XX The present invention relates to a method of preparing a genetically

XX modified organism of the genus Blakeslea, which comprises first

XX transforming at least one cell then optionally homokaryotizing the cells

XX so that cells are produced in which the nuclei are all simultaneously

XX altered in one or more genetic characteristics and these alterations are

XX expressed, and finally selection and culture of the modified cell(s). The

XX genetically modified organisms are used for the production of

XX carotenoids, particularly carotenes and xanthophylls, useful as animal

XX and human nutrients, or supplements, cosmetics and pharmaceuticals,

XX particularly for pigmentation or colouring beverages, but also as

XX antioxidants. The present sequence is a coding sequence shown in the

XX exemplification of the invention.

XX Sequence 729 BP; 103 A; 244 C; 231 G; 151 T; 0 U; 0 Other;

Query Match 95.8%; Score 698.6; DB 13; Length 729;

Best Local Similarity 97.4%; Pred. No. 1e-146; Mismatches 19; Indels 0; Gaps 0;

Matches 710; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

1 ATGAGGCGACATGCGCTGCGCCCAAGGAGATCTGACCGCCACCGATTGATCGTGGGGC 60

1 ATGAGGCGACATGCGCTGCGCCCAAGGAGATCTGACCGCCACCGATTGATCGTGGGGC 60

61 GGCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 120

61 GGCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 120

61 GGCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 120

121 GGCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 180

121 GGCATCATGCGCGATGCGCTGCGCCCTGATGTCATGCGCTGCTGAGCGCGG 180

QY 181 TTCATCATCGCGCATGACGCGATGCGTGGTGGTGGCGCGCGCGCCCAT 240
DB 181 TTCATCATCGCGCATGACGCGATGACGCGTGGTGGTGGCGCGCGCCCAT 240
QY 241 GGGGGGATGGGCGACCTTGTCTGTGGCTGTATGGCGGATTTTCTGGCGCAAGTATG 300
DB 241 GGGGGGATGGGCGACCTTGTCTGTGGCTGTATGGCGGATTTTCTGGCGCAAGTATG 300
QY 301 GTCAAGACATGAGCCATCATGCGCATGCGGACCGAGACCGACGACCATTTTCCACCAT 360
DB 301 GTCAAGACATGAGCCATCATGCGCATGCGGACCGAGACCGACGACCATTTTCCACCAT 360
QY 361 GGGCGGCGCGGTCCGTGTGACCGCCGCTTTCATCGGACCTATTTTGGCTGGCGAGGAG 420
DB 361 GGGCGGCGCGGTCCGTGTGACCGCCGCTTTCATCGGACCTATTTTGGCTGGCGAGGAG 420
QY 421 CTGGCTGCTGCGCGTGTATGCGGTATGCGGTATGCGGTATGCGGTATGCGGTATG 480
DB 421 CTGGCTGCTGCGCGTGTATGCGGTATGCGGTATGCGGTATGCGGTATGCGGTATG 480
QY 481 GTGGCTTCTTGGCGCGTGTGCGATGCGGTGCGGTGCGATGCGGTGCGGTGCGATG 540
DB 481 GTGGCTTCTTGGCGCGTGTGCGATGCGGTGCGGTGCGATGCGGTGCGGTGCGATG 540
QY 541 TGGCTGCGCGACCGCGCGCGCGCGACGACGCGGTTCGCGACCGACATGCGCGGTGCG 600
DB 541 TGGCTGCGCGACCGCGCGCGCGCGACGACGCGGTTCGCGACCGACATGCGCGGTGCG 600
QY 601 CGGATCAGGAGACCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 660
DB 601 CGGATCAGGAGACCGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 660
QY 661 CACCACTGSCACCGGACCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 720
DB 661 CACCACTGSCACCGGACCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 720
QY 721 ACCGCATGA 729
DB 721 ACCGCATGA 729

RESULT 9
ADO61156
ID ADO61156 strand; DNA; 729 BP.
AC ADO61156;
XX 15-JUL-2004 (first entry)
DT XX
DE A. aurantiacum ketolase DNA.
XX ds; ketocarotenoid; plant; ketolase; petal; flower-specific promoter;
KW petal-specific promoter; epsilon-cyclase; ec; chromoplast; hydroxylase;
KW beta-cyclase; bc; astaxanthin; canthaxanthin; adonixanthin;
KW adonixanthin; ornamental; food; animal feed; supplement; pigment;
KW colouring; trout; salmon; shrimp; gene.
OS Agrobacterium aurantiacum.
XX Key Location/Qualifiers
FH 1..729
FT CDS /tag= a
FT /product= "ketolase"
XX
XX DE10238978-A1.
XX 04-MAR-2004.
XX 20-AUG-2002; 2002DE-01038978.
XX 20-AUG-2002; 2002DE-01038978.
XX
XX (SUNG-) SUNGENE GMBH & CO KGAA.

XX WP1; 2004-215840/21.
DR P-PSDB; ADO61157.
XX
PT Method for preparing ketocarotenoids, useful e.g. as food or feed
PT supplements, by increasing, or introducing, ketolase activity in the
PT fruits of transgenic plants, also new nucleic acid constructs.
XX
PS Disclosure; SEQ ID NO 5; 77bp; German.
XX
CC This invention describes a novel method for preparing ketocarotenoids by
CC culturing genetically modified plants that, in comparison with the wild-
CC type, have altered ketolase activity in the fruits. The invention also
CC describes a nucleic acid construct comprising a fruit-specific promoter
CC linked functionally to a sequence that encodes the altered ketolase,
CC genetically modified plants in which the fruits have altered ketolase
CC activity and method for preparing such plants. The plants contain at
CC least one nucleic acid sequence that encodes the ketolase, especially
CC under control of a fruit-specific promoter, and particularly they contain
CC chromoplasts in the fruit. The ketolase-encoding nucleic acid is inserted
CC by standard methods, then the transgenic plants are cultivated, harvested
CC and ketocarotenoids are isolated from their fruits. Preferred carotenoids
CC include astaxanthin, canthaxanthin, echinenone (or its 3- or 3'-hydroxy
CC derivatives) adonixanthin or adonixanthin. The modified plants with
CC increased ketolase activity are used as ornamentals as food or animal
CC feed and for preparation of ketocarotenoids-containing extracts or for
CC preparing food/feed supplements, e.g., especially where the
CC ketocarotenoid is astaxanthin, as a pigment for colouring trout, salmon
CC and shrimps. The transgenic plants produce fruits with increased content
CC of ketocarotenoids. The invention describes a construct, vector p53XEN02
CC which comprises, in pSDUs, a cassette containing the constitutive double
CC 35S cauliflower mosaic virus promoter; the rbcS chloroplast transit
CC peptide; the ketolase gene from Haemococcus pluvialis and a terminator.
CC It was used to transform tomato cells, using Agrobacterium tumefaciens,
CC and the infected cells regenerated to plants conventionally. One of the
CC resulting transgenic lines, CS13-24, produced fruits that contained
CC lycopene, beta-carotene, canthaxanthin, adonixanthin or astaxanthin, but
CC the last three were absent from wild-type fruits (which additionally
CC contained lutein, not detected in transgenic fruits).
XX
SQ Sequence 729 BP; 103 A; 249 C; 229 G; 148 T; 0 U; 0 Other;
Query Match 95.6%; Score 697; DB 12; Length 729;
Best Local Similarity 97.3%; Pred. No. 2.3e-146;
Matches 709; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGAGCGACATGCG 60
DB 1 ATGAGCGACATGCG 60
QY 61 GGCATCATGCG 120
DB 61 GGCATCATGCG 120
QY 121 GCGCATCCCATCTGCG 180
DB 121 GCGCATCCCATCTGCG 180
QY 181 TTCATCATGCG 240
DB 181 TTCATCATGCG 240
QY 241 GGGCGATGGGCGACCTTGTCTGTGGCTGTATGGCGGATTTTCTGGCGCAAGTATG 300
DB 241 GGGCGATGGGCGACCTTGTCTGTGGCTGTATGGCGGATTTTCTGGCGCAAGTATG 300
QY 301 GTCAAGACATGAGCCATCATGCGCATGCGGACCGAGACCGACGACCATTTTCCACCAT 360
DB 301 GTCAAGACATGAGCCATCATGCGCATGCGGACCGAGACCGACGACCATTTTCCACCAT 360
QY 361 GGGCGGCGCGGTCCGTGTGACCGCCGCTTTCATCGGACCTATTTTGGCTGGCGAGGAG 420
DB 361 GGGCGGCGCGGTCCGTGTGACCGCCGCTTTCATCGGACCTATTTTGGCTGGCGAGGAG 420

PI Matuschek M, Heinekamp T, Schmidt A, Brakhage A;
 XX WPI: 2004-54087/52.
 DR P-PSDB; ADR03938.
 PT Preparing genetically modified *Blakeslea*, useful for preparation of
 PT carotenoids, useful as food additives, cosmetics or pharmaceuticals,
 XX comprises transformation, optional homokaryotizing, and selection.
 PS Disclosure; SEQ ID NO 15; 459bp; German.
 XX
 CC The present invention relates to a method of preparing a genetically
 CC modified organism of the genus *Blakeslea*, which comprises first
 CC transforming at least one cell then optionally homokaryotizing the cells
 CC so that cells are produced in which the nuclei are all simultaneously
 CC altered in one or more genetic characteristics and these alterations are
 CC expressed, and finally selection and culture of the modified cell(s). The
 CC genetically modified organisms are used for the production of
 CC carotenoids, particularly carotenes and xanthophylls, useful as animal
 CC and human nutrients, or supplements, cosmetics and pharmaceuticals,
 CC particularly for pigmentation or colouring beverages, but also as
 CC antioxidants. The present sequence is a coding sequence shown in the
 CC exemplification of the invention.
 XX
 SQ Sequence 729 BP; 103 A; 249 C; 229 G; 148 T; 0 U; 0 Other;
 Query Match 95.6%; Score 697; DB 13; Length 729;
 Best Local Similarity 97.3%; Pred. No. 2,3e-146;
 Matches 709; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ATGAGGCGACATGCCCTGCGCAAGGCGATGACCGCCAGCATTTGATGCTTCGAGC 60
 DB 1 ATGAGGCGACATGCCCTGCGCAAGGCGATGACCGCCAGCATTTGATGCTTCGAGC 60
 QY 61 GGCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 120
 DB 61 GGCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 120
 QY 61 GGCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 120
 DB 61 GGCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 120
 QY 121 GGCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 180
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 QY 121 GGCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 180
 DB 121 GGCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 180
 QY 181 TTTCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 240
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 QY 181 TTTCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 240
 DB 181 TTTCATCATGCCCGCGGTGCGCTGCGATGTCATGCGCTGCTGTTTGAGCGGCG 240
 QY 241 GGGGCGATGGGCGACGCTTCTGTCGCTGTAATGCCGATTTTCTGCGGCGAATGATC 300
 DB 241 GGGGCGATGGGCGACGCTTCTGTCGCTGTAATGCCGATTTTCTGCGGCGAATGATC 300
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 DB 241 GGGGCGATGGGCGACGCTTCTGTCGCTGTAATGCCGATTTTCTGCGGCGAATGATC 300
 QY 301 GTCAAGACATGGCCCATCATGCGCGGAAACCGACGACCCAGATTTCACAT 360
 DB 301 GTCAAGACATGGCCCATCATGCGCGGAAACCGACGACCCAGATTTCACAT 360
 QY 301 GTCAAGACATGGCCCATCATGCGCGGAAACCGACGACCCAGATTTCACAT 360
 DB 301 GTCAAGACATGGCCCATCATGCGCGGAAACCGACGACCCAGATTTCACAT 360
 QY 361 GCGCGCGCGGTGCGCTGTAACGCGGCTTCATGCGCACTATTTCGGTGGCGAGGG 420
 DB 361 GCGCGCGCGGTGCGCTGTAACGCGGCTTCATGCGCACTATTTCGGTGGCGAGGG 420
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 DB 361 GCGCGCGCGGTGCGCTGTAACGCGGCTTCATGCGCACTATTTCGGTGGCGAGGG 420
 QY 421 CTGCTGCTGCGCTGATGTAACGCTTAATGCGGTAATGTTGGGGATGCTGATGTC 480
 DB 421 CTGCTGCTGCGCTGATGTAACGCTTAATGCGGTAATGTTGGGGATGCTGATGTC 480
 QY 421 CTGCTGCTGCGCTGATGTAACGCTTAATGCGGTAATGTTGGGGATGCTGATGTC 480
 DB 421 CTGCTGCTGCGCTGATGTAACGCTTAATGCGGTAATGTTGGGGATGCTGATGTC 480
 QY 481 GTGGCTTGTGGCGGCTTGGCGTGAATCTGGGCGTGAATCAGCTGTTCTGGCGATC 540
 DB 481 GTGGCTTGTGGCGGCTTGGCGTGAATCTGGGCGTGAATCAGCTGTTCTGGCGATC 540
 QY 481 GTGGCTTGTGGCGGCTTGGCGTGAATCTGGGCGTGAATCAGCTGTTCTGGCGATC 540
 DB 481 GTGGCTTGTGGCGGCTTGGCGTGAATCTGGGCGTGAATCAGCTGTTCTGGCGATC 540
 QY 541 TGGCTGCGCGACCGCGCGCGCGACGAGCGGTTCCCGGACCGGCAATCGCGGCTGTCG 600
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 QY 601 CGGATCAGGACCGCGGTGCTGCTGATCCTGTTCACTTTGGCGGTTATCATCGAA 660
 DB 601 CGGATCAGGACCGCGGTGCTGCTGATCCTGTTCACTTTGGCGGTTATCATCGAA 660

QY 661 CACCACTGACACCGACCGGTGCTGTCGCGCTGCCAGACCCGACCAAGGGGAC 720
 DB 661 CACCACTGACACCGACCGGTGCTGTCGCGCTGCCAGACCCGACCAAGGGGAC 720
 QY 721 ACCGATGA 729
 DB 721 ACCGATGA 729
 RESULT 14
 AA099485
 ID AA099485 standard; DNA; 639 BP.
 XX
 AC AA099485;
 XX
 DT 27-AUG-2003 (revised)
 DT 28-FEB-1996 (first entry)
 XX
 DE 3 hydroxy-beta-ionone ring methylene to keto converting peptide DNA.
 XX
 KW Xanthophyll; astaxanthine; methylene; keto group; conversion;
 XX 3-hydroxy-beta-ionone ring, de.
 XX
 OS Agrobacterium aurantiacum.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..639
 FT /*tag= a
 FT /product= "beta-ionone_ring_4-methylene_to_4-keto
 FT _group_converting_polypeptide."
 XX
 W09518220-A1.
 XX
 PD 06-JUL-1995.
 XX
 PF 26-DEC-1994; 94WO-JP002220.
 XX
 PR 27-DEC-1993; 93JP-00348737.
 PR 05-SEP-1994; 94JP-00235917.
 XX
 PA (KIRI) KIRIN BEER KK.
 PA (MARI-) MARINE BIOTECHNOLOGY INST CO LTD.
 PI Misawa N, Kondo K, Kajiwara S, Yokoyama A;
 XX
 DR WPI: 1995-246386/32.
 DR P-PSDB; AAR79058.
 PT DNA's encoding xanthophyll(s) - esp. asta:xanthin and other
 PT xanthophyll(s) using e.g. E. coli.
 XX
 PS Claim 2; Page 76-78; 131pp; Japanese.
 XX
 CC Q999485-AA099485 encode xanthophyll polypeptides. These polypeptides are
 CC capable of converting the 4-methylene group of a 3-hydroxy-beta-ionone
 CC ring to a 4-keto group in doing so these peptides also add a hydroxyl
 CC group to the 3-position carbon-atom of the 4-keto-beta-ionone ring. The
 CC DNA sequences may be used in the production of astaxanthine and other
 CC keto gp. contg. xanthophylls, the sequences may also be used to transform
 CC certain yeasts and other microorganisms. (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX
 SQ Sequence 639 BP; 88 A; 215 C; 204 G; 132 T; 0 U; 0 Other;
 Query Match 83.9%; Score 611.8; DB 2; Length 639;
 Best Local Similarity 97.3%; Pred. No. 2.6e-127;
 Matches 622; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 QY 91 GTGCATGGCGTGTGTTCTGGAAGCGGCGGCGATCCATCTGGCGGTGCGCAATTTC 150
 DB 1 GTGCATGGCGTGTGTTCTGGAAGCGGCGGCGATCCATCTGGCGGTGCGCAATTTC 150

Oy		151	CTGGGAGCTACCTCGGTGTCGGTCCGATCTGTTCAATCAGCGATGAACGGATGCANTGGG	210
Dd		61	CTGGGGCTAACCTGCTGCTCGGTCCGATGTTTATCATGCCGATGAACGGATGCANTGGG	120
Oy		211	TGGGTGTCGCGGGGGCCCGCGCGCAATTGCGCGCATGGGCGAGCTTGTCCTGTGGCTG	270
Dd		121	TGGGTGTCGCGGGGGCGTCCGCGCGCAATTGCGCGCATGGGCGAGCTTGTCCTGTGGCTG	180
Oy		211	TATGCCGATTTTTCTGCGGGCAAGATGCTCAACAGCACATGGCCATCATGCCCATGGC	330
Dd		181	TATGCCGATTTTTCTGCGGGCAAGATGCTCAACAGCACATGGCCATCATGCCCATGGC	240
Oy		331	GGAACCGACGACGACCAGATTTCGACCAATGGCGGCCCCGGTCCGCTGTACGGCCGCTTC	390
Dd		241	GGAACCGACGACGACCAGATTTCGACCAATGGCGGCCCCGGTCCGCTGTACGGCCGCTTC	300
Oy		391	ATCGGACACTATTTTCGCTGCGCGCGAAGGGGCTGCTGTCGCCGTCATTCGTGAAGTCTAT	450
Dd		301	ATCGGACACTATTTTCGCTGCGCGCGAAGGGGCTGCTGTCGCCGTCATTCGTGAAGTCTAT	360
Oy		451	GCGCTGATGTTGGGGGATGGCTGATGTAAGTGTCTTCTGAGCGGTTCGGCTGATCTTG	510
Dd		361	GCGCTGATGTTGGGGGATGGCTGATGTAAGTGTCTTCTGAGCGGTTCGGCTGATCTTG	420
Oy		511	GCGTGCATTCACACTGTTGCTGTTTCGGGCATCTGSCCTCCGACCGCCCCTGGACGACGG	570
Dd		421	GCGTGCATTCACACTGTTGCTGTTTCGGGCATCTGSCCTCCGACCGCCCCTGGACGACGG	480
Oy		571	TTCGCGGACCGGACCAATGCGCGGTGTCGCGGATGACGACCCCGTGTGCTGCTGACCG	630
Dd		481	TTCGCGGACCGGACCAATGCGCGGTGTCGCGGATGACGACCCCGTGTGCTGCTGACCG	540
Oy		631	TGCTTTCACTTTGGCGGTTATCATCAAGAACACACACTGTGACCCGAGCGTGGCTTGGTGG	690
Dd		541	TGCTTTCACTTTGGCGGTTATCATCAAGAACACACACTGTGACCCGAGCGTGGCTTGGTGG	600
Oy		691	CGCCTGCCGACGACCCGCGACCAAGGGGGACACCGCATGA	729
Dd		601	CGCCTGCCGACGACCCGCGACCAAGGGGGACACCGCATGA	639
<hr/>				
RESULT 15				
AAV84074				
ID	AAV84074	standard;	DNA; 639 BP.	
AC	AAV84074;			
XX				
DT	10-MAR-1999	(first entry)		
DE	Carotenoid biosynthesis gene crtW.			
XX				
KW	Carotenoid biosynthesis; astaxanthin diglucoside; crtB gene; crtB gene;			
KM	carotenoid glycoside; crtY gene; crtZ gene; crtX gene; crtW gene;			
KM	Food additive; ds.			
XX				
OS	Agrobacterium aurantiacum.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	1..639		
FT		/tag= a		
PJ	JPI0327865-A.			
PD	15-DEC-1998.			
PF	29-MAY-1997;	97JP-00140460.		
PR	29-MAY-1997;	97JP-00140460.		
PA	(KIRI) KIRIN BREWERY KK.			
PA	(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.			
XX				

DR WPI; 1999-099030/09.

DR P-PSDB; AAW87882.

PT New carotenoid glucoside(s) - used as food additives

PS Disclosure; Page 10-11; 26pp; Japanese.

CC The preheat sequence encodes a protein involved in carotenoid
CC biosynthesis. The specification describes astaxanthin diglucosides and
CC adonixanthin-3'-glucosides. The specification also describes a method for
CC the preparation of a carotenoid glycoside, in which all, or part of,
CC carotenoid biosynthesis genes *crtb*, *crtB*, *crtI*, *crtY*, *crtZ*, *crtX* or *crtW*
CC are introduced to a microbe or plant and expressed. The transformed
CC organism is cultured and astaxanthin diglucosides, adonixanthin-3'-
CC glucosides, and/or astaxanthin monoglucoside are collected. The
CC carotenoid glucosides are used as food additives

SQ Sequence 639 BP; 88 A; 215 C; 204 G; 132 T; 0 U; 0 Other;

Query Match	83.9%;	Score 611.8;	DB 2;	Length 639;
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Matches 622; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

91 GTGATGCGCTGTGTTCTGACGCGGCGCATCCCATCCTTGGCGTCCGAATTTC 150

Db . 1 GTGCATGCGCTGTGTTTCTGACGCAGCGCGCATCCCATCCTGGCGATCGCAATTTC 60

151 CTGGGCTGACCTGGCTGCGTGGTCTGTTCAATCATCGCGCATGACCGATGCAATGGG 210

Db 61 CTGGGGCTGACCTGGCTGTGGTCGGATTGTTCATCATCGCGCATGACCGCATGCACGG 120

211 TCGGTCGTCGCGCGCCCGCCCAATGCGCGATGGCCAGCTTGTCTGTGCTG 270

Db 121 TCGGTGTGCCGGCGCTCCGGCGCCATGCGCGATGGCCAGCTTGTCTGTGCTG 180

271 TATGCCGATTTCCTGGCGCAGATGATCGTCAAGCACATGGCCCATGCC 330

Db 181 TATGCCGATTTCGTGGCGCAGATGATCGTCAAGCACATGGCCCATGC 240

331 GGAACCGACGACGCCAGATTTCGACCATGGCGGCCGGTCCGCTGTACGCCCGCTTC 390

Db 241 GGAACCGACGACGCCGATTTCGACCATGGCGGCCGCTCCGCTGTACGCCCGCTTC 300

391 ATCGCACCTATTGCGCTGGCGGAGGGCTGCTGCCCGTCATCGTGACGGTCTAT 450

Db 301 ATCGGACCTATTTCGGCTGGCGGAGGGCTGCTGCTGCCCGTCATCGTGACGGTCTAT 360

451 GCGCTGATGTTGGGGATCGCTGGATGTACGTGCTTCTGGCCGTTGCCGTGATCCTG 510

Db 361 GCGCTGATCCCTTGGGATCGCTGATGTACGTGGTCTTCTGCGCGCTGCCGTGCATCCTG 420

511 GCGTCGATCCAGCTGTTGTTGCGATCTGGCTGCCGACGCCCGGCCACGACGG 570

Db 421 GCGTCGATCCAGCTGTTGTTGCGGACCTGGCTGCCGACCGC.CCCGGCCACGACGG 480

571 TTCCCGACCGCCACAATGCGGGTCTGCGCGATCAGGACCCCGTGTGCTGCTGACC 630

Db 481 TTCCCGACCGCCACATGCGCGGTGCTGCGCGATCAGCGACCCCGTGTGCTGTGACC 540

631 TGCTTCACTTGGCGTTATCATCAGACACCACTGCACCCGACGGTGCCTTGGTGG 690

Db 541 TGCTTCACTTTGGCGTTATCATCAGACACCACTGCACCCGACGGTGCCGTGTGG 600

691 CGCCTGCCAGCACCCGCACCAAGGGGACACCGCATGA 729

Db 601 CGCCTGCCCAAGACCCGCAACCAAGGGGACACCGCATGA 639

Search completed: June 21, 2005, 20:32:42
Job time : 479.072 secs

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OY 361 GAGGAGCCGGTCCGCTGTAACGCCCGCTTCATCGGACCTATTTCCGCTGCGGAGG 420
DB 361 GAGGAGCCGGTCCGCTGTAACGCCCGCTTCATCGGACCTATTTCCGCTGCGGAGG 420
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DB 421 CTGCTGCTGCGCGTCACTGTGACCGGTCTATGCGCTGATGTTGGGGATCGCTGATGAC 480
OY 481 GTGGCTCTTGGCGCGTGTGCGATCCCTGCGGCTGATCCAGCTGTGCTGTTCCGCTGAC 540
DB 481 GTGGCTCTTGGCGCGTGTGCGATCCCTGCGGCTGATCCAGCTGTGCTGTTCCGCTGAC 540
OY 541 TGGCTGCGGACCGCGCGGACCGACGAGGCTTCCGACCGGACCAATGCGGCTGAC 600
DB 541 TGGCTGCGGACCGCGCGGACCGACGAGGCTTCCGACCGGACCAATGCGGCTGAC 600
OY 601 CGGATCAGGACCGCGGTGTGCTGCTGACCTGCTTTCACTTTGGCGTTATCATCAGAA 660
DB 601 CGGATCAGGACCGCGGTGTGCTGCTGACCTGCTTTCACTTTGGCGTTATCATCAGAA 660
OY 661 CACCACTGACACCGGAGGCTGTGTTGGCGCTGACCGACCGGACCGGAGGAG 720
DB 661 CACCACTGACACCGGAGGCTGTGTTGGCGCTGACCGACCGGACCGGAGGAG 720
OY 721 ACCGCATGA 729
DB 721 ACCGCATGA 729
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RESULT 2
US-08-980-832-30
; Sequence 30, Application US/08980832B
; Patent No. 6291204
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Teygankov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/08/980,832B
; CURRENT FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Alcaligenes PC-1
US-08-980-832-30
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Query Match 100.0%; Score 729; DB 3; Length 1261;
Best Local Similarity 100.0%; Pred. No. 9,7e-167;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGCGACATGCGCTGCGCAAGGAGATCTGACCGGACCAAGTTTATGCTTCGAGC 60
DB 40 ATGAGCGACATGCGCTGCGCAAGGAGATCTGACCGGACCAAGTTTATGCTTCGAGC 99
OY 61 GGCATCATGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 120
DB 100 GGCATCATGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 159
OY 121 GGCATCATGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 180
DB 160 GGCATCATGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 219
OY 181 TTTCATCATGCGCGATGACCGGATGATGAGGTGCTGCTGCGGAGCGCGCGCAAT 240
DB 220 TTTCATCATGCGCGATGACCGGATGATGAGGTGCTGCTGCGGAGCGCGCGCAAT 279
OY 241 GGGGCGATGGGCGAGCTTGTCTGTGCTGTATGCGGAAATTTCTGCGGCAAGATGATC 300
DB 280 GGGGCGATGGGCGAGCTTGTCTGTGCTGTATGCGGAAATTTCTGCGGCAAGATGATC 339
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OY 301 GTCAAGCATAGGCCCATCATCGCCATGCGGAAACGACGACGACCCAGATTTGACCAT 360
DB 340 GTCAAGCATAGGCCCATCATCGCCATGCGGAAACGACGACGACCCAGATTTGACCAT 399
OY 361 GAGGAGCCGGTCCGCTGTAACGCCCGCTTCATTCGGACCTATTTCCGCTGCGGAGG 420
DB 400 GAGGAGCCGGTCCGCTGTAACGCCCGCTTCATTCGGACCTATTTCCGCTGCGGAGG 459
OY 421 CTGCTGCTGCGCGTCACTGTGACCGGTCTATGCGCTGATGTTGGGGATCGCTGATGAC 480
DB 460 CTGCTGCTGCGCGTCACTGTGACCGGTCTATGCGCTGATGTTGGGGATCGCTGATGAC 519
OY 481 GTGGCTCTTGGCGCGTGTGCGATCCCTGCGGCTGATCCAGCTGTGCTGTTCCGCTGAC 540
DB 520 GTGGCTCTTGGCGCGTGTGCGATCCCTGCGGCTGATCCAGCTGTGCTGTTCCGCTGAC 579
OY 541 TGGCTGCGGACCGCGCGGACCGACGAGGCTTCCGACCGGACCAATGCGGCTGAC 600
DB 580 TGGCTGCGGACCGCGCGGACCGACGAGGCTTCCGACCGGACCAATGCGGCTGAC 639
OY 601 CGGATCAGGACCGCGGTGTGCTGCTGACCTGCTTTCACTTTGGCGTTATCATCAGAA 660
DB 640 CGGATCAGGACCGCGGTGTGCTGCTGACCTGCTTTCACTTTGGCGTTATCATCAGAA 699
OY 661 CACCACTGACACCGGAGGCTGTGTTGGCGCTGACCGACCGGACCGGAGGAG 720
DB 700 CACCACTGACACCGGAGGCTGTGTTGGCGCTGACCGACCGGACCGGAGGAG 759
OY 721 ACCGCATGA 729
DB 760 ACCGCATGA 768
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RESULT 3
US-09-920-923B-30
; Sequence 30, Application US/09920923B
; Patent No. 6677134
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Teygankov, Yuri
; TITLE OF INVENTION: Fermentative Carotenoid Production
; FILE REFERENCE: 15464 US (C38435/125944)
; CURRENT APPLICATION NUMBER: US/09/920,923B
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Alcaligenes PC-1
US-09-920-923B-30
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Query Match 100.0%; Score 729; DB 4; Length 1261;
Best Local Similarity 100.0%; Pred. No. 9,7e-167;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGAGCGACATGCGCTGCGCAAGGAGATCTGACCGGACCAAGTTTATGCTTCGAGC 60
DB 40 ATGAGCGACATGCGCTGCGCAAGGAGATCTGACCGGACCAAGTTTATGCTTCGAGC 99
OY 61 GGCATCATGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 120
DB 100 GGCATCATGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 159
OY 121 GGCATCATGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 180
DB 160 GGCATCATGCGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 219
OY 181 TTTCATCATGCGCGATGACCGGATGATGAGGTGCTGCTGCGGAGCGCGCGCAAT 240
DB 220 TTTCATCATGCGCGATGACCGGATGATGAGGTGCTGCTGCGGAGCGCGCGCAAT 279
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QY	241	GGGGGGGATGGGGCAGCTGTCCGTGGGCGTATAGCCGAAATTTTCMGGGGCAAGATGATC	300
Db	280	GGGGGGAATGGGCGAGCTTGTCCGTGGGCGTATAGCCGAAATTTTCMGGGGCAAGATGATC	339
QY	301	GTCAGACACATGGCCCATCATGCGCATGCGGAAACGACAGACAGACCAGATTTTCAGCAAT	360
Db	340	GTCAGACACATGGCCCATCATGCGCATGCGGAAACGACAGACAGACCAGATTTTCAGCAAT	399
QY	361	GGGGGCGCGGTCCGCTGGTAGCGCCCGCTTCATCGGACCTAATTTGGGCTGGCGCGAGGGG	420
Db	400	GGGGGCGCGGTCCGCTGGTAGCGCCCGCTTCATCGGACCTAATTTGGGCTGGCGCGAGGGG	459
QY	421	CTGCTGCTGCCCCGTATCTGTACAGGTCTATAGCGCTATGTTGGGGGAGATGCTGTGATGTAC	480
Db	460	CTGCTGCTGCCCCGTATCTGTACAGGTCTATAGCGCTATGTTGGGGGAGATGCTGTGATGTAC	519
QY	481	GTGCTCTCTGGCCCGTGGCCGTGCATCTGAGGCGTGATCCAGTGTTCGTTCGGGCATC	540
Db	520	GTGCTCTCTGGCCCGTGGCCGTGCATCTGAGGCGTGATCCAGTGTTCGTTCGGGCATC	579
QY	541	TGGCTGCGGACCGGCCCGCCGACGACGACGAGCTTCCCGAACCGGCACATATGCGCGGTGCG	600
Db	580	TGGCTGCGGACCGGCCCGCCGACGACGAGCTTCCCGAACCGGCACATATGCGCGGTGCG	639
QY	601	CGGATCAGCGACCCCGGTGTGCTGCTGACCTGTCTTCACTTTGGCGGTTATATCAAGAA	660
Db	640	CGGATCAGCGACCCCGGTGTGCTGCTGACCTGTCTTCACTTTGGCGGTTATATCAAGAA	699
QY	661	CACCACTGACACCCGACCGGTGCTTGTGTGGCGCTGTCCGACGACCCGACACAAAGGGGAC	720
Db	700	CACCACTGACACCCGACCGGTGCTTGTGTGGCGCTGTCCGACGACCCGACACAAAGGGGAC	759
QY	721	ACCGCATGA 729	
Db	760	ACCGCATGA 768	

RESULT 4
 US-08-663-310-7
 Sequence 7, Application US/08663310
 Patent No. 5811273
 GENERAL INFORMATION:
 APPLICANT: MISAWA, No. 5811273jhko
 APPLICANT: KONDO, Keiji
 APPLICANT: KAJIWARA, Susumu
 APPLICANT: YOKOYAMA, Akihito
 TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
 TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/663,310
 FILING DATE: 23-SEP-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/JP94/02220
 FILING DATE: 26-DEC-1994
 PRIOR APPLICATION DATA: JP 6-235917
 APPLICATION NUMBER: JP 6-235917
 FILING DATE: 05-SEP-1994

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? PRIOR APPLICATION DATA.
? APPLICATION NUMBER: JP 5-348737
? FILING DATE: 27-DEC-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 49441/1090
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202)672-5300
? TELEFAX: (202)672-5399
? TELEX: 904136
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2886 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? OS-08-663-310-7

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Query Match	95.6%	Score 697;	DB 1;	Length 2886;
Similarity	97.3%;	Pred. No. 6	4e-159;	
Matches 709;	Conservative	0;	Mismatches 20;	Indels 0;
				Gaps 0;

Qy	I	ATGAGGCCACATGCGCCCTGCCAAGGCGAGATCTGCACCGCACAGTTTATATGCTCTCGGGC	60
Db	139	ATGAGGCCACATGCGCCCTGCCAAGGCGAGATCTGCACCGCACAGTTTATCTCTCGGGC	198
Qy	61	GGCATCATGCGCGCGTGGCTGGCCCTGCATGTGCATGCGCTGTGTGTTCTTGACACCGGGC	120
Db	199	GGCATCATGCGCGCGTGGCTGGCCCTGCATGTGCATGCGCTGTGTGTTCTTGACACCGAGG	258
Qy	121	GCGCATCCCATCTCTGGCGGTTCGCGAATTTCTTGGGGCTGAACCTTGCCTGTCCGTCCGTCTG	180
Db	259	GCGCATCCCATCTCTGGCGGTTCGCGAATTTCTTGGGGCTGAACCTTGCCTGTCCGTCTCGAATTG	318
Qy	181	TTTCATCATTCGCGCATGACGCGATGATGGTTCGTCGCGGGCGCCCGCGCCCAT	240
Db	319	TTTCATCATTCGCGCATGACGCGATGATGGTTCGTCGCGGGCGTCGCCGCGCCCAT	378
Qy	241	GCGGCATTGGGCGCCAGCTTGTCTCTGGCTGTATGCGGATTTCTCTGGCGCAAGATGATC	300
Db	379	GCGGCATTGGGCGCCAGCTTGTCTCTGGCTGTATGCGGATTTCTCTGGCGCAAGATGATC	438
Qy	301	GTCAAGACATGAGCCCATCATCGGCATGCGGAAACCGACGACGACCCAGATTTCACACAT	360
Db	439	GTCAAGACATGAGCCCATCATCGGCATGCGGAAACCGACGACCCAGATTTCACACAT	498
Qy	361	GAGCGCCCGGTGCGCTGGTAGCGCCGCTTCAATCGGACCTAATTTTCGCTGGCGCGAGGGG	420
Db	499	GAGCGCCCGGTGCGCTGGTAGCGCCGCTTCAATCGGACCTAATTTTCGCTGGCGCGAGGGG	558
Qy	421	CTGCTGTGCCCCGTCACTGTGACGGTCTATGCGCTGATGTGGGGGATTCGCTGATGTAC	480
Db	559	CTGCTGTGCCCCGTCACTGTGACGGTCTATGCGCTGATGTGGGGGATTCGCTGATGTAC	618
Qy	481	GTTGCTTCTTGTGGCGGTGGCCGTGCATCTTGGCGCTGCATCCAGCTGTTTGCTGTTCCGACATC	540
Db	619	GTTGCTTCTTGTGGCGGTGGCCGTGCATCTTGGCGCTGCATCCAGCTGTTTGCTGTTCCGACATC	678
Qy	541	TGGCTGCGCGACCGCGCCCGGCGACGAGCGGTTCGCGACCGGCACAATGCGCGGTGCTGC	600
Db	679	TGGCTGCGCGACCGCGCCCGGCGACGAGCGGTTCGCGACCGGCACAATGCGCGGTGCTGC	738
Qy	601	CGGATTCAGCGACCCCGGTGTCGCTGTGACCTTGCTTTCATTGTGGCGGTTATCATCAGAA	660
Db	739	CGGATTCAGCGACCCCGGTGTCGCTGTGACCTTGCTTTCATTGTGGCGGTTATCATCAGAA	798
Qy	661	CACCACTTCGACCCGACGGTGCTTGTGTGGCGCTGCCAGACCCGACCCAGAGGGGAGC	720
Db	799	CACCACTTCGACCCGACGGTGCTTGTGTGGCGCTGCCAGACCCGACCCAGAGGGGAGC	858
Qy	721	ACCGCATGGA 729	

APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2886 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-335-919-7

Query Match 95.6%; Score 697; DB 3; Length 2886;
Best Local Similarity 97.3%; Pred. No. 6,4e-159;
Matches 709; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

1 ATGAGCGCAATCCCTGCGCCAGAGAGATCTGACCGCCACAGTTGATCGTCTGGGC 60
139 ATGAGCGCAATCCCTGCGCCAGAGAGATCTGACCGCCACAGTTGATCGTCTGGGC 198
61 GGCATATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 120
199 GGCATATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 258
121 GGCATATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 180
259 GGCATATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 318
181 TTCATATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 240
319 TTCATATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 378
241 GCGCGATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 300
379 GCGCGATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 438
301 GTCACACATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGC 360
439 GTCACACATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGC 498
361 GCGCGATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 420
499 GCGCGATGCGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 558
421 CTGCTGCTGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 480
559 CTGCTGCTGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 618
481 GTGCTGCTGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 540
619 GTGCTGCTGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 678
541 TGGCTGCTGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 600
679 TGGCTGCTGCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 738
601 CGGATCAGCGACCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGC 660
739 CGGATCAGCGACCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGC 798

661 CACCACTGACCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 720
799 CACCACTGACCGCGTGGCTGGCCCTGATGTCATGCGCTGTTGTCGACGCGCGC 858
721 ACCGATGA 729
859 ACCGATGA 867

RESULT 7

US-08-663-310-1
Sequence 1, Application US/08663310
Patent No. 5811273
GENERAL INFORMATION:
APPLICANT: MISAWA, No. 5811273hiko
APPLICANT: KONO, Keiji
APPLICANT: KAJIWARA, Suenmu
APPLICANT: YOKOYAMA, Akihiro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 639 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..636
NAME/KEY: mat peptide
LOCATION: 1..636
US-08-663-310-1

Query Match 83.9%; Score 611.8; DB 1; Length 639;
Best Local Similarity 97.3%; Pred. No. 1.6e-138;
Matches 622; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Oy      9  GTGATGACGGCTGATGATTTTCGAGACGGGGGGGGGACATCCCATCTGGACGGTGGCAATTTG  150
Db      1  GTGATGACGGCTGATGATTTTCGAGACGGGGGGGGGACATCCCATCTGGACGGTGGCAATTTG  60

Oy      151 CTGGGCGTGAACCTGGCTGTTCGGTTCGTTTCATCATTCGGCATGACGGCATG  210
Db      61  CTGGGCGTGAACCTGGCTGTTCGGTTCGTTTCATCATTCGGCATGACGGCATG  120

Oy      211 TCGGTCTGTGCGGGGGGGGGCCCGGGCGCATATGGCGGATATGGGCTCACTTGTCTTGCTG  270
Db      121  TCGGTGTGTGCGGGGGGGGGCTCGGGCGCAATATGGGGATATGGGCGCACTTGTCTTGCTG  180

Oy      271  TATGCGGATTTTTCCTGGCGCAAGATGATCTCTCAAGACATATGACCCATATCGGCATGCG  330
Db      181  TATGCGGATTTTTCCTGGCGCAAGATGATCTCTCAAGACATATGACCCATATCGGCATGCG  240

Oy      331  GGAACCGACGACGACACCCCAATTTTCACATATGCGGGCCCGGTCCTGGTATGAGCCGCTTC  390
Db      241  GGAACCGACGACGACACCCCAATTTTCACATATGCGGGCCCGGTCCTGGTATGAGCCGCTTC  300

Oy      391  ATCGGACACTTATTTTCGGCTGGCGGCGCGGAGGGGCTGCTGCTGCGCGTATGTATCGGTAT  450
Db      301  ATCGGACACTTATTTTCGGCTGGCGGCGGAGGGGCTGCTGCTGCGCGTATGTATCGGTAT  360

Oy      451  GCGCTGATGTATGGGGGGATCGCTGGATGTACGTATCTTCTGGCGGTTGCGCTGCATCTG  510
Db      361  GCGCTGATCTTATGGGGATGCTGATGATGTACGTATCTTCTGGCGGTTGCGCTGCATCTG  420

Oy      511  GCGTCGATCCAGCTGTTGCTGTTTCGGCATCTGATCCGCGCACCGCCCGGACGACGCG  570
Db      421  GCGTCGATCCAGCTGTTGCTGTTTCGGCATCTGATCCGCGCACCGCCCGGACGACGCG  480

Oy      571  TTCCCGGACCGCCACAATGGCGGCTGTGTGGGATTCAGAGAACCCCGTGTGCTGTACCC  630
Db      481  TTCCCGGACCGCCACAATGGCGGCTGTGTGGGATTCAGAGAACCCCGTGTGCTGTACCC  540

Oy      631  TGCTTTTCACTTTGGCGGTTATCATTCAGAAACAACACTGCACCCGATCGCTTTGGTGG  690
Db      541  TGCTTTTCACTTTGGCGGTTATCATTCAGAAACAACACTGCACCCGATCGCTTTGGTGG  600

Oy      691  CGCCTGCGCAGCACCCGCGACCAAGGGGGACACCGCATGA  729
Db      601  CGCCTGCGCAGCACCCGCGACCAAGGGGGACACCGCATGA  639

RESULT 8
US-09-006-491-1
: Sequence 1, Application US/09006491
: Patent No. 5972690
: GENERAL INFORMATION:
:   APPLICANT: MISHA, No. 5972690hiko
:   APPLICANT: KONDO, Keiji
:   APPLICANT: KAJIWARA, Susumu
:   APPLICANT: YOKOYAMA, Akihito
:   TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
:   TITLE OF INVENTION: XANTHOPYLLIS AND THE PROCESS FOR PRODUCING THE
:   TITLE OF INVENTION: XANTHOPYLLIS
:   NUMBER OF SEQUENCES: 12
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Foley & Lardner
:   STREET: 3000 K Street, N.W., Suite 500
:   CITY: Washington
:   STATE: D.C.
:   COUNTRY: USA
:   ZIP: 20007-5109
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patentin Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/006,491
:

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1	FLILING DATE:	
2	CLASSIFICATION:	
3	PRIOR APPLICATION DATA:	
4	APPLICATION NUMBER:	US 08/663,310
5	FILING DATE:	23-SEP-1996
6	APPLICATION NUMBER:	WO PCT/JP94/02220
7	FILING DATE:	26-DEC-1994
8	PRIOR APPLICATION DATA:	
9	APPLICATION NUMBER:	JP 6-235917
10	FILING DATE:	05-SEP-1994
11	PRIOR APPLICATION DATA:	
12	APPLICATION NUMBER:	JP 5-348737
13	FILING DATE:	27-DEC-1993
14	ATTORNEY/AGENT INFORMATION:	
15	NAME:	BENT, Stephen A.
16	REGISTRATION NUMBER:	29,768
17	REFERENCE/DOCKET NUMBER:	49441/109
18	TELECOMMUNICATION INFORMATION:	
19	TELEPHONE:	(202)672-5300
20	TELEFAX:	(202)672-5399
21	TELEX:	904136
22	SEQUENCE CHARACTERISTICS:	
23	LENGTH:	639 base pairs
24	TYPE:	nucleic acid
25	STRANDEDNESS:	double
26	TOPOLOGY:	linear
27	FEATURE:	
28	NAME/KEY:	CDS
29	LOCATION:	1..636
30	FEATURE:	
31	NAME/KEY:	mat_peptide
32	LOCATION:	1..636
33	US-09-006-491-1	
34	Query Match	83.9%; Score 611.8; DB 2; Length 639;
35	Best Local Similarity	97.3%; Pred. No. 1.6e-138;
36	Matches 622; Conservative	0; Mismatches 17; Indels 0; Gaps 0
37	91	GTGATGCGCTGTGTGTTCTGACCGCGGCGCATCCCATCTTGCGCGGATTTTC
38	1	GTGATGCGCTGTGTGTTCTGACCGCGGCGCATCCCATCTTGCGCGGATTTTC
39	151	CTGGGGCTGACCTGCTGCTGCTGTCTGTTCAATTCGCGCAAGACCGATGCGG
40	61	CTGGGGCTGACCTGCTGCTGCTGTCTGTTCAATTCGCGCAAGACCGATGCGG
41	211	TCGCTGCGCGGGGCGCGCGCGCGCCCAATCGCGGATGCGGCGCAAGCTTCTGTG
42	121	TCGCTGCGCGGGGCGCGCGCGCGCCCAATCGCGGATGCGGCGCAAGCTTCTGTG
43	271	TATGCGGATTTTCTGTGCGCAAGTATGTCACCAAGCAATGCGCCCATATGCGCAT
44	181	TATGCGGATTTTCTGTGCGCAAGTATGTCACCAAGCAATGCGCCCATATGCGCAT
45	331	GGAACCGACGACGACCCGATTTGACCATGAGCGGCGCGGTCGCTGGATGCGCGCTTC
46	241	GGAACCGACGACGACCCGATTTGACCATGAGCGGCGCGGTCGCTGGATGCGCGCTTC
47	391	ATCGGACCTATTTTCGCTGCGCGCGGAGGGCTGCTGCGCCGTCATCGTGAAGTAT
48	301	ATCGGACCTATTTTCGCTGCGCGCGGAGGGCTGCTGCGCCGTCATCGTGAAGTAT
49	451	GCGCTGATGTTGGGGGATTCGCTGATATGATGCTGCTTCTGCGCGTTCGCGCATTCG
50	361	GCGCTGATGTTGGGGGATTCGCTGATATGATGCTGCTTCTGCGCGTTCGCGCATTCG
51	511	GCGTGCATCCAGCTGTTGTTGCTGCGCATCTGCGCGCACCGCGCCCGGACGCGG
52	421	GCGTGCATCCAGCTGTTGTTGCTGCGCATCTGCGCGCACCGCGCCCGGACGCGG
53	571	TTCCCGACCGCCCAATGCGCGGCTGTCGCGGATCAGCGACCCCGTGTGCTGCTACG


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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5339
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726
NAME/KEY: mat peptide
LOCATION: 1..726
US-08-663-310-8

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Query Match      59.3%; Score 432.4; DB 1; Length 729;
Best Local Similarity 77.6%; Pred. No. 3,6e-95;
Matches 523; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 56 CGGGGGGATCATCGCCGGGTGGGCGCCCTGATGATGCGGTGCTTTCGACG 115
DB 56 CGCGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 115
QY 116 CGGCGCGCATCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 175
DB 116 CGGCGCGCATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 175
QY 176 GTCTGTTCATCATCGCGCATGACGCGCATGATGAGTGGTGGTGGCGCGCGCG 235
DB 176 GGTCTGTTCATCATCGCGCATGACGCGCATGATGAGTGGTGGTGGCGCGCGCG 235
QY 236 CCAATCGCGCATGAGCGCGCATGAGCGCGCATGAGCGCGCATGAGCGCGCATG 295
DB 236 CCAATCGCGCATGAGCGCGCATGAGCGCGCATGAGCGCGCATGAGCGCGCATG 295
QY 296 TGATGTCGACGACATGAGCGCGCATGAGCGCGCATGAGCGCGCATGAGCGCGCAT 355
DB 296 TGATGTCGACGACATGAGCGCGCATGAGCGCGCATGAGCGCGCATGAGCGCGCAT 355
QY 356 ACCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 415
DB 356 GTACGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 415
QY 416 AGGGGCTGTGCTGCGCCGCTGATGAGCGGTCTATGCGGTGATGTTGGGGATTCG 475
DB 416 AGGGAATGCTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 475
QY 476 TGTAGTGTCTTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 535
DB 476 TGTATGTATCTTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 535
QY 536 GCATCTGCTGCGCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 595

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DB 536 GAACCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 595
QY 596 CGTGGCGGATGAGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 655
DB 596 CGACCGGATGAGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 655
QY 656 AGGAACACCACTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 715
DB 656 AGGAACATCACTGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 715
QY 716 GAGACACCGCATGA 729
DB 716 GAGCGCGCGCATGA 729

RESULT 11
US-09-006-491-8
Sequence 8, Application US/09006491
Patent No. 5972690
GENERAL INFORMATION:
APPLICANT: MISAWA, No. 5972690jnhko
APPLICANT: KAJIWARA, Susumu
APPLICANT: KONDO, Keiji
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,491
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5339
TELEX: 904136
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..726

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Db      356 GTCAAGAGGAGGCGCGTGTGTACAGGAGCGTCTGTCCACTATTTCGGCTGGCAG 415
QY      416 AGGGGTGTGTGTGCGCCGTCATCGTACGAGTGTATGCGTATGTTGGGGATCGCTGA 475
Db      416 AGGAACTGTGCTACCGGTGATGTACCACTATGCGTATCTTGGCGATCCCTGGA 475
QY      476 TGTACGTGTCTTTCGCGCGTGTGCGTGTGATCTGCGCGTGTGATCCAGCTGTGTGTCG 535
Db      476 TGTATGTATCTTTCGCGCGGTGTGCGCGGTGTGCGCGTGTGATCCAGATTTTGTGTCG 535
QY      536 GCATCTGCTGCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 595
Db      536 GAACCTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 595
QY      596 CGTGGCGATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 655
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RESULT 13

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US-08-663-310-12
; Sequence 12, Application US/08663310
; Patent No. 5811273
; GENERAL INFORMATION:
; APPLICANT: MISAWA, No. 5811273ihiko
; APPLICANT: KONDO, Keiji
; APPLICANT: KAJIWARA, Susumu
; APPLICANT: YOKOYAMA, Akihito
; TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
; TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,310
; FILING DATE: 23-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/02220
; FILING DATE: 26-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-235917
; FILING DATE: 05-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-348737
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 49441/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136

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; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-663-310-12

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Query Match      59.3%; Score 432.4; DB 1; Length 1631;
Best Local Similarity 77.6%; Pred. No. 4,3e-95;
Matches 523; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

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RESULT 14

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US-09-006-491-12
; Sequence 12, Application US/09006491
; Patent No. 5972690
; GENERAL INFORMATION:
; APPLICANT: MISAWA, No. 5972690ihiko
; APPLICANT: KONDO, Keiji
; APPLICANT: KAJIWARA, Susumu
; APPLICANT: YOKOYAMA, Akihito
; TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
; TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-09-335-919-12

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Best Local Similarity	77.6%	Pred No. 4.3e-95		
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Qy	596	CGTCCGCGGATCAGGGAACCCGTGTGCTGTACCGGCTTCATCTTTGGCGGTATATC	655
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Job time : 198.419 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: June 21, 2005, 22:57:55 ; Search time 524.43 Seconds
(without alignments)
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Title: US-10-695-980-31

Perfect score: 729

Sequence: 1 atgagcgcacatcgcctgc.....ccaagggggacacccgacga 729

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	729	100.0	729	15	US-10-166-225A-180
2	729	100.0	729	18	US-10-695-980-31
3	729	100.0	1261	10	US-09-920-923-30
4	729	100.0	1261	18	US-10-695-980-30
5	697	95.6	729	22	US-10-997-844-31
6	533.8	73.2	756	22	US-10-997-844-7
7	383.8	52.6	726	9	US-09-547-267-11

8	383.8	52.6	726	10	US-09-920-923-28	Sequence 28, Appl
9	383.8	52.6	726	18	US-10-695-980-28	Sequence 28, Appl
10	217	29.8	777	14	US-10-166-037-1	Sequence 1, Appl
11	195.4	26.8	735	18	US-10-466-656-38	Sequence 38, Appl
12	195.4	26.8	735	21	US-10-848-307-38	Sequence 38, Appl
13	69.2	9.5	1761	9	US-09-791-687A-1	Sequence 1, Appl
14	69.2	9.5	1761	9	US-09-791-687A-2	Sequence 2, Appl
15	69.2	9.5	1761	9	US-09-791-687A-3	Sequence 3, Appl
16	66.2	9.1	1458	10	US-09-920-923-31	Sequence 31, Appl
17	58.8	8.1	825	17	US-10-369-493-40591	Sequence 40591, A
18	52.4	7.2	1038	17	US-10-310-154-95	Sequence 95, Appl
19	52.4	7.2	1038	21	US-10-732-923-210	Sequence 210, Appl
20	52.4	7.2	1091	21	US-10-947-979-47	Sequence 47, Appl
21	51.2	7.0	522	15	US-10-156-761-3323	Sequence 3323, Appl
22	51.2	7.0	9025608	15	US-10-156-761-1	Sequence 1, Appl
23	50.4	6.9	1189	17	US-10-260-228-3770	Sequence 3770, Appl
24	49.8	6.8	741	15	US-10-156-761-4808	Sequence 4808, Appl
25	49.8	6.8	1431	17	US-10-282-122A-7249	Sequence 7249, Appl
26	49.8	6.8	9025608	15	US-10-156-761-1	Sequence 1, Appl
27	49.8	6.7	3131	17	US-10-282-122A-7241	Sequence 7241, Appl
28	49.8	6.7	13029	9	US-09-815-242-4052	Sequence 4052, Appl
29	49.8	6.7	13029	17	US-10-282-122A-7240	Sequence 7240, Appl
30	48.6	6.7	1243	18	US-10-425-114-24278	Sequence 24278, A
31	48.6	6.7	2031	17	US-10-369-493-42813	Sequence 42813, A
32	48.6	6.6	1618	18	US-10-425-114-35569	Sequence 35569, A
33	48.6	6.6	1732	20	US-10-425-115-109983	Sequence 109983, A
34	48.6	6.6	3183	17	US-10-282-122A-14200	Sequence 14200, A
35	47.4	6.5	3178	19	US-10-437-963-47749	Sequence 47749, A
36	47.4	6.4	873	20	US-10-425-115-183240	Sequence 183240, A
37	46.6	6.4	2421	20	US-10-425-115-145240	Sequence 145240, A
38	46.2	6.3	669	19	US-10-437-963-44697	Sequence 44697, A
39	46.2	6.3	2002	19	US-10-437-963-68831	Sequence 68831, A
40	46.2	6.3	798	15	US-10-156-761-10337	Sequence 30337, Appl
41	46.2	6.3	2238	19	US-10-437-963-97363	Sequence 97363, A
42	46.2	6.3	10692	15	US-10-156-761-414	Sequence 414, Appl
43	45.8	6.3	10000	21	US-10-156-761-15103	Sequence 15103, A
44	45.8	6.3	1102	21	US-10-947-979-7	Sequence 7, Appl
45	45.8	6.3	1102	21	US-10-947-979-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-166-225A-180
; Sequence 180, Application US/10166225A
; Publication No. US20030148416A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETEL, Warner
; APPLICANT: HUMBERT, Markus
; APPLICANT: LOPEZ-DUIBARI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/10/166,225A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patent version 3.1
; SEQ ID NO 180
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Paracoccus carotinifaciens F-396
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(726)
; OTHER INFORMATION: Beta-carotene Beta-4 oxygenase
US-10-166-225A-180

Query Match 100.0%; Score 729; DB 15; Length 729;
Best Local Similarity 100.0%; Pred. No. 6.3e-197;
Matches 729; Conservative 0; Mismatches 0; Gaps 0;

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      1 ATGAGGACATAGCCCTGCGCCAAAGGAGATGTGACCGGACCAAGTTGATCGTCTCGGGC 60
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QY      61 GGCATCATGCGCGCGTGGCTGGCCCTGATGTGATGCGCTGTGGTTCTGGACCGGCG 120
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QY      301 GTCAAGCATATGGCCCATATGCGGCAATGCGGAAACCGAGACCAAGATTTGACCAT 360
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; Sequence 31, Application US/10695980
; Publication No. US20040058410A1
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tsyanankov, Yuri
; TITLE OF INVENTION: Fermentative Carotenoid Production
; FILE REFERENCE: 15464 US (38435/125944)
; CURRENT APPLICATION NUMBER: US/10/695,980
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US/09/920,923B
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 729
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ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: E-396
US-10-695-980-31
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Best Local Similarity 100.0%; Pred. No. 6.3e-197;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; APPLICANT: Tsyanankov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/09/920,923
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;; PRIOR FILING DATE: 1997-12-01
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;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 30
;; LENGTH: 1261
;; TYPE: DNA
;; ORGANISM: Alcaligenes PC-1
US-09-920-923-30

Query Match 100.0%; Score 729; DB 10; Length 1261;
Best Local Similarity 100.0%; Pred. No. 6.7e-197;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGCATATGCTCTGCCCAAGGAGATCTGACCCGCCACCGTTTGATCTGCTGGGC 60
DB ATGAGCGCATATGCTCTGCCCAAGGAGATCTGACCCGCCACCGTTTGATCTGCTGGGC 99
QY 61 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 120
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 159
QY 121 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 180
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 219
QY 160 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 240
DB TTTCATATGCGCGCATATGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 279
QY 241 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 300
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 339
QY 280 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 360
DB GTCAAGCATATGCGCGCATATGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 399
QY 340 GTCAAGCATATGCGCGCATATGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 420
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 459
QY 361 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 480
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 519
QY 421 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 540
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 579
QY 460 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 600
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 639
QY 541 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 660
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 699
QY 601 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 720
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 759
QY 661 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 780
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 819
QY 721 ACCGATGA 729
DB ACCGATGA 768

RESULT 4
US-10-695-980-30
; Sequence 30, Application US/10695980
; Publication No. US20040058410A1
; GENERAL INFORMATION:

;; APPLICANT: Pasamontes, Luis
;; APPLICANT: Teyankov, Yuri
;; TITLE OF INVENTION: Fermentative Carotenoid Production
;; FILE REFERENCE: 15464 US (C38435/125944)
;; CURRENT APPLICATION NUMBER: US/10/695,980
;; CURRENT FILING DATE: 2003-10-29
;; PRIOR APPLICATION NUMBER: US/09/920,923B
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: 08/980,832
;; PRIOR FILING DATE: 1997-12-01
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 30
;; LENGTH: 1261
;; TYPE: DNA
;; ORGANISM: Alcaligenes PC-1
US-10-695-980-30

Query Match 100.0%; Score 729; DB 18; Length 1261;
Best Local Similarity 100.0%; Pred. No. 6.7e-197;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGCATATGCTCTGCCCAAGGAGATCTGACCCGCCACCGTTTGATCTGCTGGGC 60
DB ATGAGCGCATATGCTCTGCCCAAGGAGATCTGACCCGCCACCGTTTGATCTGCTGGGC 99
QY 61 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 120
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 159
QY 121 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 180
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 219
QY 160 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 240
DB TTTCATATGCGCGCATATGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 279
QY 241 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 300
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 339
QY 280 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 360
DB GTCAAGCATATGCGCGCATATGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 399
QY 301 GTCAAGCATATGCGCGCATATGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 420
DB GTCAAGCATATGCGCGCATATGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 459
QY 340 GTCAAGCATATGCGCGCATATGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 480
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 519
QY 361 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 540
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 579
QY 421 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 600
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 639
QY 460 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 660
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 699
QY 541 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 720
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 759
QY 601 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 780
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 819
QY 661 GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 840
DB GGCATATGCGCGCGTGGGCTGGGCTGCAATGTCATGCGCTGCTGTTCTGAGCGGGC 879
QY 721 ACCGATGA 729
DB ACCGATGA 768

RESULT 5
US-10-997-844-31
; Sequence 31, Application US/10997844
; Publication No. US20050124033A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Pamela L
; APPLICANT: Bosak, Melissa
; APPLICANT: Tao, Luan
; APPLICANT: Sedkova, Natalia
; APPLICANT: Cheng, Qiong L
; TITLE OF INVENTION: Optimized Bacterial Host Strains of Methylobionas sp. 16A
; FILE REFERENCE: CL-2230 US NA
; CURRENT APPLICATION NUMBER: US/10/997,844
; PRIOR FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/527,083
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/527,877
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Agrobacterium aurantiacum
US-10-997-844-31

Query Match 95.6%; Score 697; DB 22; Length 729;

Best Local Similarity 97.3%; Pred. No. 7,7e-186; Mismatches 20; Indels 0; Gaps 0;

Matches 709; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 ATGAGCGACATGCGCTGCGCAAGGAGATCTGACCGCAGCAAGTTGATCGTCTCGGCG 60
DB 1 ATGAGCGACATGCGCTGCGCAAGGAGATCTGACCGCAGCAAGTTGATCGTCTCGGCG 60
QY 61 GGCATATCGCGCGCTGCGCTGCGCTGCGATGTCATGCGCTGCTGCTGCGACGCGCG 120
DB 61 GGCATATCGCGCGCTGCGCTGCGCTGCGATGTCATGCGCTGCTGCTGCGACGCGCG 120
QY 121 GGGCATCCCATCTGCGCGCTGCGCAATTCCTGCGCGCTGCACTGCGCTGCGCTGCG 180
DB 121 GGGCATCCCATCTGCGCGCTGCGCAATTCCTGCGCGCTGCACTGCGCTGCGCTGCG 180
QY 181 TTTCATCATGCGCGATGACCGGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 240
DB 181 TTTCATCATGCGCGATGACCGGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 240
QY 241 GCGCGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GCGCGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 GTCAAGCAATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGAT 360
DB 301 GTCAAGCAATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGAT 360
QY 361 GCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 420
DB 361 GCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 420
QY 421 CTGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 CTGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 GTGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 GTGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 TGGCTGCGCGACCG 600
DB 541 TGGCTGCGCGACCG 600
QY 601 CGGATCAGGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660

DB 601 CGGATCAGGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 CACCACTGCGACCG 720
DB 661 CACCACTGCGACCG 720
QY 721 ACCGCATGA 729
DB 721 ACCGCATGA 729

RESULT 6

US-10-997-844-7
; Sequence 7, Application US/10997844
; Publication No. US20050124033A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Pamela L
; APPLICANT: Bosak, Melissa
; APPLICANT: Tao, Luan
; APPLICANT: Sedkova, Natalia
; APPLICANT: Cheng, Qiong L
; TITLE OF INVENTION: Optimized Bacterial Host Strains of Methylobionas sp. 16A
; FILE REFERENCE: CL-2230 US NA
; CURRENT APPLICATION NUMBER: US/10/997,844
; PRIOR FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/527,083
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/527,877
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon-optimized crtw gene from Agrobacterium aurantiacum
US-10-997-844-7

Query Match 73.2%; Score 533.8; DB 22; Length 756;
Best Local Similarity 83.3%; Pred. No. 1.6e-141; Mismatches 122; Indels 0; Gaps 0;

Matches 607; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 1 ATGAGCGACATGCGCTGCGCAAGGAGATCTGACCGCAGCAAGTTGATCGTCTCGGCG 60
DB 22 ATGAGCGCGCAATGCGCTGCGCAAGGAGATCTGACCGCAGCAAGTTGATCGTCTCGGCG 81
QY 61 GGCATATGCGCGCGCTGCGCTGCGCTGCGATGTCATGCGCTGCTGCTGCGACGCGCG 120
DB 61 GGCATATGCGCGCGCTGCGCTGCGCTGCGATGTCATGCGCTGCTGCTGCGACGCGCG 120
QY 82 GGCATATGCGCGCGCTGCGCTGCGCTGCGATGTCATGCGCTGCTGCTGCGACGCGCG 141
DB 82 GGCATATGCGCGCGCTGCGCTGCGCTGCGATGTCATGCGCTGCTGCTGCGACGCGCG 141
QY 121 GGGCATCCCATCTGCGCGCTGCGCAATTCCTGCGCGCTGCACTGCGCTGCGCTGCG 180
DB 121 GGGCATCCCATCTGCGCGCTGCGCAATTCCTGCGCGCTGCACTGCGCTGCGCTGCG 180
QY 142 GGCATCCCATCTGCGCGCTGCGCAATTCCTGCGCGCTGCACTGCGCTGCGCTGCG 201
DB 142 GGCATCCCATCTGCGCGCTGCGCAATTCCTGCGCGCTGCACTGCGCTGCGCTGCG 201
QY 181 TTTCATCATGCGCGATGACCGGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 240
DB 181 TTTCATCATGCGCGATGACCGGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 240
QY 202 TTTCATCATGCGCGATGACCGGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 261
DB 202 TTTCATCATGCGCGATGACCGGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 261
QY 241 GCGCGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 GCGCGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 262 GCGCGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321
DB 262 GCGCGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321
QY 301 GTCAAGCAATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGAT 360
DB 301 GTCAAGCAATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGAT 360
QY 322 GTCAAGCAATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGAT 381
DB 322 GTCAAGCAATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGATGCGCGAT 381
QY 361 GCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 420
DB 361 GCGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 420
QY 382 GGTGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 441
DB 382 GGTGCGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 441
QY 421 CTGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

76 TGGCTGGCCCTGACATGTCAGTCCGCTGTGTTTCTGAGACGCGGCGGCGCATCCCATCTGTG 135

CCCTG 135
|||

Db 76 TGGCTGTTCTGACGCTTTTCACCTTGCTGCTGAGCTGCTGCTACCCGCTGCTG 135
Qy 136 GGGCTGCGAATTTCTGAGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 195
Db 136 GCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 195
Qy 196 GACGCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 255
Db 196 GACGCTATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 255
Qy 256 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
Db 256 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
Qy 316 CATCATGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
Db 316 CACCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
Qy 376 TGGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
Db 376 TGGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
Qy 436 ATCGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
Db 436 ATCGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
Qy 496 TTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555
Db 496 TTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555
Qy 556 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
Db 556 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
Qy 616 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
Db 616 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
Qy 676 ACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718
Db 676 CACGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718

RESULT 9
US-10-695-980-28
; Sequence 28, Application US/10695980
; Publication No. US20040058410A1
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tsyganov, Yuri
; TITLE OF INVENTION: Fermentative Carotenoid Production
; FILE REFERENCE: 15464 US (C38435/125944)
; CURRENT APPLICATION NUMBER: US/10/695,980
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US/09/920,923B
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Alicaligenes PC-1
US-10-695-980-28

Query Match 52.6%; Score 383.8; DB 18; Length 726;
Best Local Similarity 74.8%; Pred. No. 6.1e-99;
Matches 481; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

Qy 76 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 135
Db 76 TGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 135

Qy 136 GGGCTGCGAATTTCTGAGGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 195
Db 136 GCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 195
Qy 196 GACGCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 255
Db 196 GACGCTATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 255
Qy 256 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
Db 256 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
Qy 316 CATCATGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
Db 316 CACCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
Qy 376 TGGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
Db 376 TGGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
Qy 436 ATCGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
Db 436 ATCGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
Qy 496 TTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555
Db 496 TTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555
Qy 556 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
Db 556 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
Qy 616 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
Db 616 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
Qy 676 ACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718
Db 676 CACGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718

RESULT 10
US-10-166-037-1
; Sequence 1, Application US/10166037
; Publication No. US2003008737A1
; GENERAL INFORMATION:
; APPLICANT: GIRAUD, Eric
; APPLICANT: HANNIBAL, Laure
; TITLE OF INVENTION: Isolated Carotenoid biosynthesis gene cluster involved
; FILE REFERENCE: 1721-55
; CURRENT APPLICATION NUMBER: US/10/166,037
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/297,272
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: crtlw
US-10-166-037-1

Query Match 29.8%; Score 217; DB 14; Length 777;
Best Local Similarity 61.3%; Pred. No. 1.3e-51;
Matches 425; Conservative 0; Mismatches 250; Indels 18; Gaps 4;

Qy 21 CAGGCAATGCTGACCGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 80
Db 51 CGATGCGAGGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 110

LENGTH: 735
TYPE: DNA
ORGANISM: Brevundimonas aurantiaca
US-10-848-307-38

Query Match 26.8%; Score 195.4; DB 21; Length 735;
Best Local Similarity 59.8%; Pred. No. 1.8e-45;
Matches 407; Conservative 0; Mismatches 256; Indels 18; Gaps 4;

QY 31 CTGACCGCACAGTTGATCGTCGCGCGGCATCATCGCGCGGTGCGTCCCTGCAT 90
DB 40 CAGACCTGATGCTGACCTCGCGGAGATGATGCGGAGATGCGGCTTGTGAT 99
QY 91 GTGCAATGCGCTGATTTCTGAGACGCGCGGCATCCCATCTGCGCGTCCGATTTTC 150
DB 100 GTCTACGGGTCTATTTCACCGATGCGGCGCTTGACCTGTGTATGCGCCCGGCGATC 159
QY 151 CTGGAG---CTGACCTGCTGTGCTGCTGCTGTCTGTTCATCATGCGCATGACGCGATGCAT 207
DB 160 GTGGCGGTTCAGACCTGGTTGTGCGGCTTTTCATGTCGCCCATGACCGCATGTAC 219
QY 208 GGTGCGTGTGCGCGCGCGCGCGCGCATATGCGCGCATGCGGCAAGTGTCTGCGTGG 267
DB 220 GACTCCCTGCGCGCGGAGCGCGCGCTGAAACGCGCATGCGCGGCTGACCTTGGAG 279
QY 268 CTGTATGCGGATTTCTGCGCGCAAGATGATGTCAGACATGAGCGCATGCGCAT 327
DB 280 CTCTATGCGGCTTCCGCTTTCATGCGGTGAAAGACGCGCACACGCCACACGCGCG 339
QY 328 GCGGAGACGACGACGACCGACAGATTTGAC-----CATGGCGCGCGGCTCCGCTGG 378
DB 340 CCGGACAGCGCGACGACCGGATTTTCAGCGCCCGCGCGCGCTTCCCTCCCTGG 399
QY 379 TAAGCCCGCTCATGCGGACCTATTGCGCGCGCGAGCGGCTGCTGTGCGCGCATC 438
DB 400 TTCTGAACTTTCTTTCGACCTATTGCGCGCGGAGATGAGCGGCTCTGACCGCGCTG 459
QY 439 GTGACGCTGATGCGGTGATGTTGGGAGATCGCTGATGTA---GTGCTCTTTCGCG 495
DB 460 GTCTGATGCGCTTCTGCGCGCTGCGGCGCGCGCGCGCAATCTCTGACCTTTCGCG 519
QY 496 TTGCGGTGATCTTGCGGTGATTCAGCTGTGTGTTGCGCATGCGCTGCGCGACCG 555
DB 520 GCGCGCGCGCTTCTTTCAGCGCTTCAGCTTTCACCTTTCGCGCATGCGCGACCG 579
QY 556 CCGGCGACGACGCGCTTCCCGGACCGCGCACATGCGCGGTGCTGCGGATCAGCGACCG 615
DB 580 CACACCGACGACCGCTTCCCGGACCGCGCACAGCGCGCGCTTACGCGCGCGCTG 639
QY 616 GTGCGCTGCTGACCTGCTTTCATCTTTCGCGGTTATCATCAGAACACCACTGACCG 675
DB 640 CTTCCTGCTGACCTGCTTTCACCTTTCGCGCG---CACACGAGAACACCATGTGAGCGCG 696
QY 676 ACGTGCCTTGTGCGCGCTG 696
DB 697 TGGCGCGCGCTGCTGCTG 717

RESULT 13

US-09-791-687A-1
Sequence 1, Application US/09791687A
Patent No. US20020053096A1
GENERAL INFORMATION:
APPLICANT: Hirschberg, Joseph
APPLICANT: Lotan, Tamar
TITLE OF INVENTION: POLYNUCLEOTIDE MOLECULE FROM HAEMATOCOCCUS PLUVIALIS ENCODING A
TITLE OF INVENTION: POLYPEPTIDE HAVING A BETA-C-4-OXYGENASE ACTIVITY FOR BIOTECHNOLO
TITLE OF INVENTION: OF (3S,3'S) ASTAXANTHIN AND ITS SPECIFIC EXPRESSION IN CHROMOBLA
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 01/21600
CURRENT APPLICATION NUMBER: US/09/791,687A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 09/259,294

PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1761
TYPE: DNA
ORGANISM: Haematococcus pluvialis
US-09-791-687A-1

Query Match 9.5%; Score 69.2; DB 9; Length 1761;
Best Local Similarity 50.7%; Pred. No. 1.3e-09;
Matches 223; Conservative 0; Mismatches 208; Indels 9; Gaps 2;

QY 139 GTGCGAATTTCTGCGGCTGACCTGCTGTGCTGTGCTGTTCATCATGCGCATGAC 198
DB 526 GTGCGAATTTCTTGTCTGCTGAGTCTGTACACAGGCTTTTATATCACCAGCATGAT 585
QY 199 GCGATGATGATGCTGTGTGCGCGCGCGCGCGCGCATATGCGCATGCGGCTG 258
DB 586 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
QY 259 GTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 318
DB 646 TGCATCTCTGTATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 705
QY 319 CATGCGCA---TGCGGAGACGACGACGACGACGACGACGACGACGACGACGACG 369
DB 706 CACACGACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 765
QY 370 GTGCGCTGTATGCGCGCTTTCATGCGGACCTATTTCGCTGCGCGCGCGCGCTG 429
DB 766 GTGCGCTGTATGCGCGCTTTCATGCGGACCTATTTCGCTGCGCGCGCGCGCTG 825
QY 430 CCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489
DB 826 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 885
QY 490 TGGCGGTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
DB 886 ATGGGCG 945
QY 550 CACG 569
DB 946 CACAGCTGAGCTGCGCG 965

RESULT 14

US-09-791-687A-2
Sequence 2, Application US/09791687A
Patent No. US20020053096A1
GENERAL INFORMATION:
APPLICANT: Lotan, Tamar
APPLICANT: Hirschberg, Joseph
TITLE OF INVENTION: POLYNUCLEOTIDE MOLECULE FROM HAEMATOCOCCUS PLUVIALIS ENCODING A
TITLE OF INVENTION: POLYPEPTIDE HAVING A BETA-C-4-OXYGENASE ACTIVITY FOR BIOTECHNOLO
TITLE OF INVENTION: OF (3S,3'S) ASTAXANTHIN AND ITS SPECIFIC EXPRESSION IN CHROMOBLA
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 01/21600
CURRENT APPLICATION NUMBER: US/09/791,687A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 09/259,294
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 1761
TYPE: RNA
ORGANISM: Haematococcus pluvialis
US-09-791-687A-2

Query Match 9.5%; Score 69.2; DB 9; Length 1761;
Best Local Similarity 37.7%; Pred. No. 1.3e-09;
Matches 166; Conservative 57; Mismatches 208; Indels 9; Gaps 2;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 19:42:50 ; Search time 2873.3 Seconds

(without alignments)
9657.484 Million cell updates/sec

Title: US-10-695-980-31

Perfect score: 729

Sequence: 1 atgagcgcacatccctcctcc.....ccaagggggacaccgatga 729

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	8.9	666	4	BG846752 1024014H0
2	55.6	7.6	925	4	CNS00091P
3	52	7.1	1201	9	CNS01690
4	50.6	6.9	1101	9	CNS0178Y
5	50	6.9	925	9	CNS00091P
6	49	6.7	849	8	CC407345
7	48.8	6.7	427	5	BQ245798
8	48.8	6.7	663	6	CA108291
9	48.4	6.6	1100	9	CNS01690
10	48.2	6.6	633	6	CA161275
11	48.2	6.6	677	6	CA161511
12	48	6.6	613	7	COS33928
13	48	6.6	785	6	CG236345
14	47.6	6.5	634	6	CA096815
15	47.2	6.5	933	4	BG343324
16	47.2	6.5	968	4	AG030603
17	47.2	6.5	1169	8	BZ561896
18	47.2	6.5	1206	9	CL971023
19	47	6.4	693	7	COS20246
20	47	6.4	906	9	CG354638
21	47	6.4	907	9	CG354627
22	46.6	6.4	946	9	CG290659
23	46.6	6.4	351	4	B1479111
24	46.6	6.4	658	6	CA247911

C 25	46.6	6.4	664	6	CA119890	CCCLR106
C 26	46.6	6.4	1101	9	CNS01258	AL101954 Drosophila
C 27	46.4	6.4	796	6	CG271311	CG1BR78TV
C 28	46.2	6.3	564	6	CB815935	CB815935 3529.1.78
C 29	46.2	6.3	813	9	CG450503	CG450503 OCTA61TV
C 30	46.2	6.3	918	9	CG643169	CG643169 OGLAR77H
C 31	46	6.3	517	2	BE400971	BE400971 AMB009.CO
C 32	46	6.3	592	7	CF132851	CF132851 WHE4351.A
C 33	46	6.3	1009	9	CNS0108W	AL098882 Drosophila
C 34	45.8	6.3	437	4	B1679572	B1679572 949003P12
C 35	45.8	6.3	524	6	CD485064	CD485064 3529.1.11
C 36	45.8	6.3	627	7	COS33576	COS33576 3530.1.22
C 37	45.8	6.3	763	7	COS26309	COS26309 3530.1.17
C 38	45.6	6.3	1366	8	BZ572253	BZ572253 msh2.2562
C 39	45.6	6.3	2082	9	CL980714	CL980714 O8IFCC045
C 40	45.4	6.2	560	7	CN887421	CN887421 010512AM
C 41	45.4	6.2	574	7	CN898104	CN898104 010701AA2
C 42	45.4	6.2	695	9	CL541678	CL541678 OB_Ba006
C 43	45.4	6.2	1005	9	CL974026	CL974026 O8IFCC042
C 44	45.2	6.2	726	9	CL963016	CL963016 O8IFCC008
C 45	45.2	6.2	811	7	CN152570	CN152570 WOUN1_82

ALIGNMENTS

RESULT 1
BG846752 666 bp mRNA linear EST 29-MAY-2001
DEFINITION 1024014H04.y1 C. reinhardtii CC-1690, normalized, lambda zap II
LOCUS BG846752
ACCESSION BG846752
VERSION BG846752.1 GI:14227936
KEYWORDS
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 666)
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J. P., Sillflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants: Project phase 2

JOURNAL Unpublished (2000)
COMMENT
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
source
Location/Qualifiers
1..666
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, lambda zap II"

/note="Vector: pBluescript II SK-; Site 1: EcoRI, Site 2: XhoI, This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in YAP (acetate-containing) medium in the light, YAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exsist (Stratagene) phage. The library was normalized using method 4 described in Bonaldi et al (1996) Genome Research 6: 791-806."

[illegible]

RESULT 4
 CNS017SY/C
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Location/Qualifiers
 1..1101

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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_1="BACN37L08"
/clone_1b="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : Sp6" .

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Query Match	Best Local Similarity	6.9%;	Score 50.6;	DB 9;	Length 1101;
Matches	42;	Conservative 158;	Mismatches 113;	Indels 0;	Gaps 0;
QY	322	CGCCATGCCGAGACGACGACCCAGATTGCACCATGCGCGCCGCTCGCTGATC	381		
Db	1069	SSSTSTSTBTBTBBSBSSBBSBBSGSSSBBSBSSSTSSSSSSSTSSSSSTSBTBTBTS	1010		
QY	382	GCCCCGTTCAATCGGACCACTATTTCGCGTCGGCGGACAGGGCGCTGCTGCCCGCTAATCGTG	441		
Db	1009	TSSSSTTTTTTTTTTTTTTTTBTBBSBSBSSSSSTSSSBRTSKBTBSBSSTSSAABS	950		
QY	442	ACGGCTATGAGCGCTGATGTTGGGGGATTCGCGATGACGTTGCTTCGCGCCGTGCGG	501		
Db	949	SSSSSSSSSSTTBTSTBBSBTSSSSSSSSSSSBBSBTBSBSBTBTBTBTBTSTSS	890		
QY	502	TCGATCCTGGCGTGCATCCAGCTTTCGTTCGTTCGCAATCTGGCTGCGCACCGCCCGGAC	561		
Db	889	SSTBTBTBBSBSSSSSSBSBSBTBTSBBSBBSYSSBSBRTSKBTSBTBTBTBTB	830		
QY	562	CACGACGCGTTCCCGGACCGCCACAAATGCGCGGCTGTCGCGAATCAGGACCCCGTTCG	621		
Db	829	MSKBSSTSTSTBTSBBSBBSGCGSCGTSBSGCSBCKRSTBSGTSSTGTTCCBBSGTGCS	770		
QY	622	CTGCTGACCTGCT	634		
Db	769	CCCTCSCCCTCTST	757		

	RESULT 5
	CNS0091P/c
LOCUS	
DEFINITION	CNS0091P 925 bp DNA linear GSS 03-JUN-1998
ACCESSION	Drosophila melanogaster genome survey sequence Tetr3 end of BAC #
VERSION	BACR15D16 of RPCI-98 library from Drosophila melanogaster (fruit
KEYWORDS	fly), genomic survey sequence.
SOURCE	AL053013
ORGANISM	AL053013.1 GI:4934461
	GSS.
	Drosophila melanogaster (fruit fly)
	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
	Ephydroidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 925)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 151 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cnm.fr - Web : www.genoscope.cnm.fr) determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoler in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's PL and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .

ORIGIN

/clone="TAEL15020A09R"
/tissue_type="developing seeds"
/dev_stage="15 days after anthesis"
/lab_host="E. coli DH10B"
/clone_lib="TAEL15"
/note="Vector: PCMV-SPORT6.0 (Invitrogen Technologies);
Site 1: NotI; Site 2: MluI; mRNA obtained from wheat seeds
of cultivar Glenlea 15 days post-anthesis"

Query Match 6.7%; Score 48.8; DB 5; Length 427;
Best Local Similarity 46.3%; Pred. No. 0.44;
Matches 161; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

214 GTGTGTCCTGGGGGCGCCGCGCATGCGCGCATGCGCGCATGCTGTGCTGTGCTGTAT 273
59 GTGCGCGAGAGGAGGCGCCGCGCGCGCGCGCGCGCTCTCTCCACGCGCTTCGCGAG 118
274 GCGCGATTTTCTGCGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 333
119 CTCTGCTCTCTCTGCGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 178
334 ACCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 393
179 GCGCGCGACGCTCGCGCGCTACGCGCGCTCGCGCGCTCGCGCGCTCGCGCGCTCGCGCGCT 238
394 GCGACCTATTTTCTGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 453
239 ATGCTCAGCTCTGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 298
454 CTGATGTTGGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 513
299 GTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 358
514 TCGATCAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561
359 GACCGGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 406

RESULT 8 663 bp mRNA linear EST 23-SEP-2003
CA108291
LOCUS SCSFHR1043A02.9 HRI Saccharum officinarum cDNA clone SCSFHR1043A02
DEFINITION 5' mRNA sequence.

ACCESSION CA108291 GI:34961598
VERSION CA108291.1
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

REFERENCE 1 (bases 1 to 663)
AUTHORS Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: pattud@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
plate: 043 row: A column: 02
Seq primer: T7 Promoter Primer.

FEATURES
source
1..663
/organism="Saccharum officinarum"
/mol_type="mRNA"

ORIGIN

/db_xref="taxon:4547"
/clone="SCSFR1043A02"
/lab_host="DH10B"
/clone_lib="HRI"
/note="Organ: seedlings inoculated with Herbaspirillum
rubrisubalbicans; Vector: pSPORT1; Site 1: SalI; Site 2:
NotI; An unidirectional cDNA library generated from
[seedlings inoculated with Herbaspirillum
rubrisubalbicans]. cDNA was prepared from poly(A+ mRNA
using Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://succest.lad.ic.unicamp.br/public"

Query Match 6.7%; Score 48.8; DB 6; Length 663;
Best Local Similarity 45.8%; Pred. No. 0.44;
Matches 167; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

214 GTGTGTCCTGGGGGCGCCGCGCATGCGCGCATGCGCGCATGCTGTGCTGTGCTGTAT 273
43 GTTGCAGGACATCTGACTGCGCGCGCTCCCTCCCTCCCTCCCTCTCTGCTCTGCTG 102
274 GCGCGATTTTCTGCGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 333
103 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 162
334 ACCGAC 393
163 GTGAAGAGACACG 222
394 GCGACCTATTTTCTGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 453
223 GTGAC 282
454 CTGATGTTGGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 513
283 AAGAGACAGGTGTGCG 342
514 TCGATCAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 573
343 AAGAGAGCTCTACGAGCGCAAGCTGTGGTCAACGATGCTGATTTCAAGAGCTC 402
574 CCGGA 578
403 CAGGA 407

RESULT 9 1100 bp DNA linear GSS 26-JUL-1999
CNS016KD
LOCUS CNS016KD
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN16D22 of Drosophila library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL106855 GI:5624152
VERSION AL106855.1
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

REFERENCE 1 (bases 1 to 1100)
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC

COMMENT
1..1100
/organism="Drosophila melanogaster"
/mol_type="DNA"

ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
1 (bases 1 to 677)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: partrud@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>
Plate: 068 row: H column: 03
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. 677
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCMRZ3068H03"
/lab_host="DH10B"
/lab_lib="R23"
/note="Organ: Shoot-root transition zone from adult plants; Vector: pSPORT; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from shoot-root transition zone from adult plants). cDNA was prepared from poly(A⁺ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucst.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 6.6%; Score 48.2; DB 6; Length 677;
Best Local Similarity 45.8%; Pred. No. 0.61; Mismatches 198; Indels 0; Gaps 0;
Matches 167; Conservative 0;

214 GTCGTCGCGGCGCGCCGCAATGCGCGCGAGCTTGTCTGTGCTGTAT 273
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71 GTTGGCGGCACTGATCGACGCGCTCCCTCCGATCGCTTCTGCTCTCTG 130
|||
274 GCCGATTTTCTGCGGCAAGATGATGTCAGACATGCGCCATCATGCCATGCCGA 333
|||
131 CTCCTGCTTCCCGCGCCCTCGCGATCGAGCAGCCATGCGCGCCACGCTCTCGCGCGC 190
|||
334 ACCGAGAGAGACCAATTTGACGACATGCGCGCGCTGCGTGAAGCGCGCTTCATC 393
|||
191 GTGAAGAGACCAACCCCGCGCGCAAGCGCGCAATCGACGCGCTCGCGCGCTTCGCT 250
|||
394 GGCACCTATTTTGGCTGCGCGCGAGGCGCTGCTCCGCTCATCGTGAAGCTCTATGCG 453
|||
251 GTGAGAGAGACCAACAAAGCGCGAGAACGCGCTCTGAGATTGCTGGCGCGTGGAGGCG 310
|||
454 CTGATTTGGGGGATGCTGATGATGATGATGATTTTCTGCGCGCTTGTGATCTGCGCG 513
|||
311 AAGGAGACAGGTGTGCGCGCGCAAGCTGACCACTTCAAGGCGCATTCGAGGCGGCG 370
|||
514 TGATTCAGCTGTGCTGCTGCGCATGCGCGCGACGCGCGCGACGAGCGGCTTC 573
|||
371 AAGAGAGAGCTCTACAGAGCGCAAGTCTGGGTCAAGCGCATGCTTCACTTCAAGAGCTC 430
|||
574 CCGGA 578
|||
431 CAGGA 435
Db

RESULT 12
COS33928
DEFINITION
COS33928 613 bp mRNA linear EST 15-JUL-2004
3530_1_223_1.G07_Y_1 3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION
COS33928
VERSION
COS33928.1 GI:50338802
KEYWORDS
EST.
SOURCE
Zea mays
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 613)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Maize ESTs from various cDNA libraries sequenced at Stanford University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530_1_223_1 row: G column: 07.
Location/Qualifiers
1. 613
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="R73"
/db_xref="taxon:4577"
/tissue_type="multiple"
/dev_stage="varies by tissue"
/lab_host="DH10B"
/clone_lib="3530 - Full length cDNA library created by
Invitrogen from multiple tissues"
/note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCMV-SHORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery Project contracted with Invitrogen to produce a normalized, full length library in a pSPORT vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the vector and sequencing primers are available at ZmDB in the EST library description tables. poly(A⁺ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20X to 80X reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the unique clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (<http://www.genome.arizona.edu/orders/>). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

ORIGIN

Query Match 6.6%; Score 48; DB 7; Length 613;
 Best Local Similarity 44.5%; Pred. No. 0.68;
 Matches 241; Conservative 0; Mismatches 295; Indels 6; Gaps 1;

QY 35 CGGCCACAGTTGATGCTGCGGGGAGATCATGCGCGGCTGCGGCTCGCATGTC 94
 |||||
 DB 29 CGCGGATGCTTGGGAGGCTGCTCGGCGGTGCGCGGATCCAGCATGCGCGCA 88
 |||||
 QY 95 ATGCGCTGCTTTCGACGCGCGCGCATCCATCCGTCGCGGAAATTTCTGG 154
 |||||
 DB 89 ACAGATGCTTTGCAAGACGCGCGCGCCGCACTCTCTGCTCTGGAAGCAGACG 148
 |||||
 QY 155 GCGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 214
 |||||
 DB 149 TCCG 208
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 QY 215 TCGTGGCG 274
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 DB 209 ACATGCGGATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 268
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 QY 275 CGGATTTTCTGCGCGCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 334
 |||||
 DB 269 CGGCGCTGCTGCG 328
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 QY 335 CGGACGACGACCCAGATTTCGACATGCGCGCGCGCGCGCGCGCGCGCGCGCG 394
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 DB 329 GCGTCTTCCCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 382
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 QY 395 GCACTATTTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 454
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 DB 383 TGAATCGGTCG 442
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 QY 455 TGATGTTGGGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 514
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 DB 443 TGTGCTGCGCGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 502
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 QY 515 CGATTCAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
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 DB 503 TGTTCGCCATGACCGGACGCTGAGCTACGCGGCGCACGCGCGCTCACGCGTTC 562
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 QY 575 CG 576
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 DB 563 AG 564
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RESULT 13
 CG236345 785 bp DNA linear GSS 22-ANG-2003
 LOCUS OGWLC52TV ZM 0.7.1.5.KB Zea mays genomic clone ZMMBMA067107,
 DEFINITION genomic survey sequence.
 ACCESSION CG236345
 VERSION CG236345.1 GI:34136231
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 785)
 Whiteley,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other_GSSs: OGWLC52TV
 COMMENT
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TP
 Class: sheared ends.

FEATURES
 source Location/Qualifiers
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 methylation filtered genomic DNA library"

ORIGIN

Query Match 6.6%; Score 48; DB 9; Length 785;
 Best Local Similarity 44.5%; Pred. No. 0.69;
 Matches 241; Conservative 0; Mismatches 295; Indels 6; Gaps 1;

QY 35 CGGCCACAGTTGATGCTGCGGGGAGATCATGCGCGGCTGCGGCTCGCATGTC 94
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 DB 209 CGCGGATGCTTGGGAGGCTGCTCGGCGGTGCGCGGATCCAGCATGCGCGCA 268
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 QY 95 ATGCGCTGCTTTCGACGCGCGCGCATCCATCCGTCGCGGAAATTTCTGG 154
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 DB 269 ACAGATGCTTTGCAAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 328
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 QY 155 GCGTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 214
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 DB 329 TCCG 388
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 QY 215 TCGTGGCG 274
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 DB 209 ACATGCGGATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 448
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 QY 275 CGGATTTTCTGCGCGCAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 334
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 DB 449 CGGCGCTGCTGCG 508
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 QY 335 CGGACGACGACCCAGATTTCGACATGCGCGCGCGCGCGCGCGCGCGCGCGCG 394
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 DB 509 GCGTCTTCCCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 562
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 QY 395 GCACTATTTCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 454
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 DB 563 TGAATCGGTCG 622
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 QY 455 TGATGTTGGGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 514
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 DB 623 TGTGCTGCGCGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 682
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 QY 515 CGATTCAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574
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 DB 683 TGTTCGCCATGACCGGACGCTGAGCTACGCGGCGCACGCGCGCTCACGCGTTC 742
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 QY 575 CG 576
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 DB 743 AG 744
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RESULT 14
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 LOCUS SCCCL6005G08.g Cl6 Saccharum officinarum cDNA clone SCCCL6005G08
 DEFINITION 5', mRNA sequence.
 ACCESSION CA096815
 VERSION CA096815.1 GI:34950122
 KEYWORDS EST.
 SOURCE Saccharum officinarum
 ORGANISM Saccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Saccharum; Saccharum officinarum
 complex.
 1 (bases 1 to 634)
 Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
 Centro de Biologia Molecular e Engenharia Genetica
 Universidade Estadual de Campinas
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil
 Tel: 55 19 3788 1137
 Fax: 55 19 3788 1089
 Email: parnuda@unicamp.br

Clone distribution: clone distribution information can be found
 through the Brazilian Clone Collection Center (BCCC) at
 http://www.bcccenter.fcav.unesp.br
 Plate: 005 row: G column: 08
 Seq primer: T7 Promoter Primer.
 Location/Qualifiers

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 /lab_host="DH10B"
 /clone_lib="CL6"
 /note="Organ: Pool of sugarcane calli submitted to low (40C) and high (37 C) temperature stress; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Pool of sugarcane calli submitted to low (40C) and high (37 C) temperature stress]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-cd columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://succest.iad.ic.unicamp.br/public"

ORIGIN

Query Match 6.5%; Score 47.6; DB 6; Length 634;
 Best Local Similarity 48.0%; Pred. No. 0.85;
 Matches 171; Conservative 0; Mismatches 179; Indels 6; Gaps 1;

QY 36 GCGCACGATTGATGTCCTCGGCGGCATCATCGCGGTGTCGCCCTGCATGTGCA 95
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 QY 96 TCGCGTGTGTTTCTGAGACGGCGCGCATCCATCCGTGGCGTGCAGATTCTCTGG 155
 DB 320 TCTGCAAGGTGTTCTGACCGGCTGACAAAGCGCGGTCTGAGATGTTCTCTGA 379
 QY 156 GCTGACCTGCTGTGCTGCTGCTGTTTCATCATCGGCATGACGGCATGATGGTCCGT 215
 DB 380 TCTTAAACAGGTGACATGACGAGGTCTATCGCCGCGCTGCTGTTGAGAGAACGC- 438
 QY 216 CGTGCAGGCGCGCGCGCGCAATGCGGCGATGGCGAGCTTGTCTGTGGCTGTATGC 275
 DB 439 -----CGAAGCCCAAGAGAGGTCAAGACCGCATGGCGCGCGCTGATCTGTGCAAGAGAA 493
 QY 276 CGGATTTTCTGGCGGAATGATGCTCAAGCAATGCGCCCATCATCGCCATCCCGGAAC 335
 DB 494 CTGGAGAGGACATCGGAAGCGCGTGCAGAGAGAGAACTTCAAGCGGAGTGGCGGCTT 553
 QY 336 CGACGACGACCGAGATTTCACCATGCGCGCGCGGTCCGCTGTACGCCCGCTTCA 391
 DB 554 CAGCAACCAACGCGCAAGCGCGCGCGCGCGCTTGGCCCTTGGCGGCGCATTTCA 609

RESULT 15 BG343324 933 bp mRNA linear EST 22-OCT-2001
LOCUS BG343324
DEFINITION HVSME90005G17f Hordeum vulgare pre-anthesis spike EST library
 HVCNDA0008 (white to yellow anther) Hordeum vulgare subsp. vulgare
 cDNA clone HVSME90005G17f, mRNA sequence.
ACCESSION BG343324
VERSION BG343324.1 GI:13155653

KEYWORDS

EST.
 Hordeum vulgare subsp. vulgare
 SOURCE
 Hordeum vulgare subsp. vulgare
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

REFERENCE

1 (bases 1 to 933)
 Wing,R., Close,T.J., Kleinofa,A., Wise,R., Begum,D., Friesch,D.,
 Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
 Fenton,R.D., Close,S.J., Oates,R. and Main,D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex pre-anthesis spike cDNA library
 Unpublished (2001)

TITLE

JOURNAL

COMMENT

Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 474
 Seq primer: AATTACCTCCTAAGCG
 High quality sequence step: 744.
 Location/Qualifiers

FEATURES

source

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 /clone="HVSME90005G17f"
 /tissue_type="pre-anthesis spike"
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 HVCNDA0008 (white to yellow anther)"
 /note="Vector: lambdaZAP; Site 1: ScaRI; Site 2: XhoI;
 Plants were grown in the greenhouse at the University of
 California, Riverside (Fenton, SJ Close, TJ Close). Whole
 spike with awns trimmed were collected at white, green and
 yellow anther stages (Fenton). Total RNA was prepared from
 each pool, equal quantities of all three RNA pools were
 combined, poly(A) RNA was purified from the mixture, one
 primary unamplified cDNA library was made, and 1 million
 pfu were in vivo excised to give plasmid SK(-) cDNA
 phagemids. These steps were performed in the TJ Close lab
 (Choi) at the University of California, Riverside.
 Phagemids were plated and picked at the Clemson University
 Genomics Institute (CUGI) (Begum, Palmer, Friesch, Atkins
 and Wing) plasmid DNA preparations, RNA sequencing and
 sequence analysis were performed at CUGI (Wing, Yu,
 Friesch, Henry, Simmons, Oates, Rambo, Main). The sequence
 has been trimmed to remove vector sequence and contains a
 minimum of 100 bases of phred value 20 or above. For more
 details on library preparation and sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders_Albo
 see Close TJ, Wing R, Kleinofa A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html)"

ORIGIN

Query Match 6.5%; Score 47.2; DB 4; Length 933;
 Best Local Similarity 46.0%; Pred. No. 1.1;
 Matches 160; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 214 GTCTGCGCGGCGCGCGCGCAATGCGGCGATGGCGCAGCTGTCTGTGCTGTAT 273
 DB 80 GTCTGCGGACGAGGCGCGCGCGCGCGCGGCTCTCTTCTCAAGCGCTTCCGAG 139
 QY 274 GCGGATTTCTCTGCGCAAGATGATCTCAAGCAATGCGCCCATCATGCGCATGCCGA 333
 DB 140 CTCTGCTCTCTGCGCGCAAGATGCGGCTCTGCGCGCGCGCGGCTTCCGCGCTTC 199

OY	241	CGCGGAGATGGGCGACCTGTTCCCTGGCTGATGACCGAGATTTTCTCGGCGCAAGATGATC	300
Db	241	CGCGGAGATGGGCGACCTGTTCTCTGGCTGATGACCGAGATTTTCTCGGCGCAAGATGATC	300
OY	301	GTCAAGCAATGAGCCCATTCATGCGCATGCGGAAACCGACGACGCCAGATTTTCGACAT	360
Db	301	GTCAAGCAATGAGCCCATTCATGCGCATGCGGAAACCGACGACGCCAGATTTTCGACCAT	360
OY	361	GGCGGCGCGGATCCGCTGGTAGGCGCGGCTTCAATCCGAGACCTAATTTGGGCTGGGCGACGGG	420
Db	361	GGCGGCGCGGATCCGCTGGTAGGCGCGGCTTCAATCCGAGACCTAATTTGGGCTGGGCGCGAGGG	420
OY	421	CTGCTGCTGCGCCGTCATCGTAGCGGCTTATGCGCTGATGTTGGGGAGATCGCTGATGTAC	480
Db	421	CTGCTGCTGCGCCGTCATCGTAGCGGCTTATGCGCTGATGTTGGGGAGATCGCTGATGTAC	480
OY	481	GTGGTCTTCTGGGCGGTTGGCCGTGCATCTCTGGGGTGCATCCACTGTTCCTGTTCCGACATC	540
Db	481	GTGGTCTTCTGGGCGGTTGGCCGTGCATCTCTGGGGTGCATCCACTGTTCCTGTTCCGACATC	540
OY	541	TGGCTGCGGACCGGCGCCGCGACACACGCGGTTCCGCGACCGGACACATGCGCGGTCGTG	600
Db	541	TGGCTGCGGACCGGCGCCGCGACACGCGGTTCCGCGACCGGACACATGCGCGGTCGTG	600
OY	601	CGGATCAGCGACCCCGGTGTCGCTGCTGACCTGCTTTCACTTTGGCGGTTATCATACGAA	660
Db	601	CGGATCAGCGACCCCGGTGTCGCTGCTGACCTGCTTTCACTTTGGCGGTTATCATACGAA	660
OY	661	CACCACTGTGACCCGACGCGTGTGCTTGTGTGGCGGCTTGCACGACCCGACACCGCAAGGGGAGC	720
Db	661	CACCACTGTGACCCGACGCGTGTGCTTGTGTGGCGGCTTGCACGACCCGACACCGCAAGGGGAGC	720
OY	721	ACCGCATGA 729	
Db	721	ACCGCATGA 729	

RESULT 2
AR452029

RESULT 2			
AR452029			
LOCUS	AR452029	729 bp	DNA
DEFINITION	Sequence 31 from patent US 6671134.		linear
ACCESSION	AR452029		
VERSION	AR452029.1	GI:42683356	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 729)		
TITLE	Paramontes, L. and Tsygankov, Y.		
JOURNAL	Fermentative carotenoid production		
FEATURES	Patent: US 6671134-A; 31-33; JAN-2004;		
	Location/Qualifiers		
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Query Match	100.0%	Score 729	DB 6	Length 729
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		Gaps	0	

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Db 1 ATGAGCGCAGCATGCCCTGCTGCCAAGGCAGATCTGACCCGCCACAGTTTGATCGTCTCGGCG 60

QY 61 GGCAATCATGCGCCGAGCTGGCCGATGTCATGCAATGCGCTGTGGATTCTGGACGGGAGG 120
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D6 61 GGCAATCATGCGCGTGGCTGGCCCTGATGTCATGCAATGCGCTGTGGATTCTGGACGGGAGG 120
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Dy 121 GCGATCCCATCTGAGGTTCGGAAATTTCCTGGGGCTACCTGGCTGCCTGGTCTTG 180

Dd 121 GCGATCCCATCTGAGGTTCGGAAATTTCCTGGGGCTACCTGGCTGCCTGGTCTTG 180

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Db	181	TTCAATCATCGCGCATGAGACGCATATGGATGGGATCGGATCGAGCGGGGCGCCGCGCGCCCAAT	240
QY	241	GGCGGATGAGGCACAGCTTGTCTCTGAGCTGTATGCGCGATTTTCTTGCGCAAGATGATC	300
Db	241	GGCGGATGAGGCACAGCTTGTCTCTGAGCTGTATGCGCGATTTTCTTGCGCAAGATGATC	300
QY	301	GTCAGACACATAGGCCCATCATTCGCCATATGCCGAACCGACGACGACACCCAGATTTTGCATC	360
Db	301	GTCAGACACATAGGCCCATCATTCGCCATATGCCGAACCGACGACGACACCCAGATTTTGCATC	360
QY	361	GGCGGCGCGGATCCGCTGGTAGCCCGCTTCATCCGSCATATTTTGCGTGCGCGCAGAGGG	420
Db	361	GGCGGCGCGGATCCGCTGGTAGCCCGCTTCATCCGSCATATTTTGCGTGCGCGCAGAGGG	420
QY	421	CTGCTGTACCCCGCTCATCGTAGCGATCTTATGCGCTGATGTTTGAGGGAGATCGCTGATGTAC	480
Db	421	CTGCTGTACCCCGCTCATCGTAGCGATCTTATGCGCTGATGTTTGAGGGAGATCGCTGATGTAC	480
QY	481	GTGGTCTTCTGAGCGGTTGCCGTGCATCTTGAGGCTGCATCAGCTGTTGCTGTTCCGCATC	540
Db	481	GTGGTCTTCTGAGCGGTTGCCGTGCATCTTGAGGCTGCATCAGCTGTTGCTGTTCCGCATC	540
QY	541	TGGCGTCCGCGACCGGCCCGGCGCACGAGCGGTTCCCGGACCGCGCAAAAGCGCGCTGTCG	600
Db	541	TGGCGTCCGCGACCGGCCCGGCGCACGAGCGGTTCCCGGACCGCGCAAAAGCGCGCTGTCG	600
QY	601	CGGATCAGCGACCCCGTGTGCTGTGCATGACTTTCATTTTGCGGCTTATCATACGAA	660
Db	601	CGGATCAGCGACCCCGTGTGCTGTGCATGACTTTCATTTTGCGGCTTATCATACGAA	660
QY	661	CACCACTTGACACCGAGCGGTGCTTGAGACTTTCATTTTGCGGCTTATCATACGAA	720
Db	661	CACCACTTGACACCGAGCGGTGCTTGAGACTTTCATTTTGCGGCTTATCATACGAA	720
QY	721	ACCGCATGA	729
Db	721	ACCGCATGA	729

RESULT 3
AX701576

RESULT 3				
AX701576				
LOCUS	AX701576	729 bp	DNA	linear
DEFINITION	Sequence 180 from Patent WO0209095.			
ACCESSION	AX701576			
VERSION	AX701576.1	GI:29537147		
KEYWORDS				
SOURCE				
ORGANISM				
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	Paracoccus carotinifaciens			
	Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;			
	Rhodobacteraceae; Paracoccus.			
REFERENCE				
AUTHORS	1 Berry, A., Bretzel, W., Huemelin, M., Lopez-Ulibarri, R., Mayer, A. F. and Yeliseev, A.			
TITLE	Improved isoprenoid production			
JOURNAL	Patent; WO 0209095-A 180 12-DEC-2002;			

FEATURES	SOURCE
ROGUE	VITAMINS AG (CN)
LOCATION/Qualifiers	1. .729

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGCAATGCGCCCTGCGCCAGAGATCTGACCCGCCAGCTTTGATCCGTCTGGGC 60
DB 1 ATGAGGGCAATGCGCCCTGCGCCAGAGATCTGACCCGCCAGCTTTGATCCGTCTGGGC 60
QY 61 GGCATCATGCGCGCGCTGCGCTGAGCTGATGTCATGCGCTGCTGCTTCTGAGCGGGCG 120
DB 61 GGCATCATGCGCGCGCTGCGCTGAGCTGATGTCATGCGCTGCTGCTTCTGAGCGGGCG 120
QY 121 GGCATCATGCGCGCGCTGCGCTGAGCTTCTGAGGGCTGACCTGCTGCTGCTGCTG 180
DB 121 GGCATCATGCGCGCGCTGCGCTGAGCTTCTGAGGGCTGACCTGCTGCTGCTGCTG 180
QY 181 TTCATCATGCGCGATGACCGGATGATGAGTGGGTGGGTGGTGGGGGGCGCGCGCCAT 240
DB 181 TTCATCATGCGCGATGACCGGATGATGAGTGGGTGGGTGGTGGGGGGCGCGCGCCAT 240
QY 241 GCGGCGATGCGCGCGCTGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 300
DB 241 GCGGCGATGCGCGCGCTGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 300
QY 301 GTCAGACATGCGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 360
DB 301 GTCAGACATGCGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 360
QY 361 GCGGCGCGCGCTGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 420
DB 361 GCGGCGCGCGCTGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 420
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DB 421 CTGCTCTGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 480
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QY 541 TGGCTGCGCGATGCGCGCGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 600
DB 541 TGGCTGCGCGATGCGCGCGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 600
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DB 601 CGGATCAGGAGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 660
QY 661 CACCACTGCAACCGGATGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 720
DB 661 CACCACTGCAACCGGATGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 720
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DB 721 ACCGATGA 729

RESULT 4

LOCUS AR169854 1261 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 30 from patent US 6291204.
ACCESSION AR169854
VERSION AR169854.1 GI:17907785
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1261)
AUTHORS Pasamontes, L. and Tsygankov, Y.

TITLE Fermentative carotenoid production
JOURNAL Patent: US 6291204-A-20-18-SEP-2001;
FEATURES
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Query Match 100.0%; Score 729; DB 6; Length 1261;
Best Local Similarity 100.0%; Pred. No. 2.9e-110;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGCAATGCGCCCTGCGCCAGAGATCTGACCCGCCAGCTTTGATCCGTCTGGGC 60
DB 40 ATGAGGGCAATGCGCCCTGCGCCAGAGATCTGACCCGCCAGCTTTGATCCGTCTGGGC 99
QY 61 GGCATCATGCGCGCGCTGCGCTGAGCTGATGTCATGCGCTGCTGCTTCTGAGCGGGCG 120
DB 100 GGCATCATGCGCGCGCTGCGCTGAGCTGATGTCATGCGCTGCTGCTTCTGAGCGGGCG 159
QY 121 GGCATCATGCGCGCGCTGCGCTGAGCTTCTGAGGGCTGACCTGCTGCTGCTGCTG 180
DB 160 GGCATCATGCGCGCGCTGCGCTGAGCTTCTGAGGGCTGACCTGCTGCTGCTGCTG 219
QY 181 TTCATCATGCGCGATGACCGGATGATGAGTGGGTGGGTGGTGGGGGGCGCGCGCCAT 240
DB 220 TTCATCATGCGCGATGACCGGATGATGAGTGGGTGGGTGGTGGGGGGCGCGCGCCAT 279
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DB 280 GCGGCGATGCGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 339
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DB 340 GTCAGACATGCGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 399
QY 361 GCGGCGCGCGCTGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 420
DB 400 GCGGCGCGCGCTGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 459
QY 421 CTGCTCTGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 480
DB 460 CTGCTCTGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 519
QY 481 GTGGTCTTCTGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 540
DB 520 GTGGTCTTCTGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 579
QY 541 TGGCTGCGCGATGCGCGCGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 600
DB 580 TGGCTGCGCGATGCGCGCGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 639
QY 601 CGGATCAGGAGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 660
DB 640 CGGATCAGGAGCGCGCTGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 699
QY 661 CACCACTGCAACCGGATGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 720
DB 700 CACCACTGCAACCGGATGCTGCTGCTGATGCGCGATTTTCTGCGCGCAAGATGATC 759
QY 721 ACCGATGA 729
DB 760 ACCGATGA 768

RESULT 5

LOCUS AR452028 1261 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 30 from patent US 6677134.
ACCESSION AR452028
VERSION AR452028.1 GI:42683355
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1261)
AUTHORS Paramontes, L. and Tsygankov, Y.
TITLE Fermentative carotenoid production
JOURNAL Patent: US 6677134-A 30 13-JAN-2004;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 729; DB 6; Length 1261;
Best Local Similarity 100.0%; Pred. No. 2.9e-110;
Matches 729; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCGCATGCCCTGCGCCAAAGGAGATCTGACCGGCAAGTTGATCGCTCGGGC 60
DB 40 ATGAGCGCATGCCCTGCGCCAAAGGAGATCTGACCGGCAAGTTGATCGCTCGGGC 99
QY 61 GGCATCATGCCCGCGTGGCGCTGAGCTGATGTCAGCTGTGTTCTGGACGCGCG 120
DB 100 GGCATCATGCCCGCGTGGCGCTGAGCTGATGTCAGCTGTGTTCTGGACGCGCG 159
QY 121 GCGCATCCCATCTGTGGCGGTGCGAAATTTCTGTGGGCTGACCTGTGTGGTCTG 180
DB 160 GCGCATCCCATCTGTGGCGGTGCGAAATTTCTGTGGGCTGACCTGTGTGGTCTG 219
QY 181 TTGATCATGGCGATGACCGGATGATGATGGGTGGTGTGCGGGGCGCCGCGCCAT 240
DB 220 TTGATCATGGCGATGACCGGATGATGATGGGTGGTGTGCGGGGCGCCGCGCCAT 279
QY 241 GCGGCGATGGGCGAGCTTGCTGTCGTGATGTCGCGAATTTCTGCGCGCAAGATGATC 300
DB 280 GCGGCGATGGGCGAGCTTGCTGTCGTGATGTCGCGAATTTCTGCGCGCAAGATGATC 339
QY 301 GTCAAGCATGAGCCCATCATGCGCATGCGGAAACCGAGCAAGCCAGATTTGACCAT 360
DB 340 GTCAAGCATGAGCCCATCATGCGCATGCGGAAACCGAGCAAGCCAGATTTGACCAT 399
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DB 640 GCGATCAGGAGCCCGGTGTGCGCTGACCTGCTTCACTTTGGCGGTTATCATCAAGAA 699
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DB 700 CACCACTTGACCGGACCGGTGCTGTGATGCGCTGACCGGACCGGACCGGAG 759
QY 721 ACCGATGA 729
DB 760 ACCGATGA 768

RESULT 6
CQ788339 CQ788339 729 bp DNA linear PAT 24-MAR-2004
LOCUS CQ788339
DEFINITION Sequence 9 from Patent WO2004018695.

ACCESSION CQ788339
VERSION CQ788339.1 GI:45723106
KEYWORDS
SOURCE Paracoccus marcusii
ORGANISM Paracoccus marcusii
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
Rhodobacteriaceae; Paracoccus.

REFERENCE
AUTHORS Schopfer, C.R., Flachmann, R., Herbers, K., Kunze, I., Sauer, M. and
Klebsattel, M.
TITLE Method for producing ketocarotenoids in plant fruit
JOURNAL Patent: WO 2004018695-A 9 04-MAR-2004;
Sungene GmbH & Co. KGaA (DE)
FEATURES Location/Qualifiers
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ORIGIN
Query Match 95.8%; Score 698.6; DB 6; Length 729;
Best Local Similarity 97.4%; Pred. No. 3.3e-105;
Matches 710; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 ATGAGCGCATGCCCTGCGCCAAAGGAGATCTGACCGGCAAGTTGATGCTCGGGC 60
DB 1 ATGAGCGCATGCCCTGCGCCAAAGGAGATCTGACCGGCAAGTTGATGCTCGGGC 60
QY 61 GGCATCATGCGCGGTGCGGCGCTGATGTCAGCTGTGTTCTGGACGCGCG 120
DB 61 GGCATCATGCGCGGTGCGGCGCTGATGTCAGCTGTGTTCTGGACGCGCG 120
QY 121 GCGCATCCCATCTGTGGCGGTGCGAAATTTCTGTGGGCTGACCTGTGTGGTCTG 180
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DB 241 GCGGCGATGGGCGAGCTTGCTGTGAGCTGTATGCGGGAATTTCTGCGCGAAGATGATC 300
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DB 361 GCGGCGCGGTGCGGTGATGCGCGCTTCATTCGGAACCTATTTGCGCTGGCGAGG 420
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QY 721 ACCGATGA 729
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RESULT 7
CQ793306 729 bp DNA linear PAT 29-MAR-2004
LOCUS CQ793306
DEFINITION Sequence 9 from Patent WO2004017749.
ACCESSION CQ793306
VERSION CQ793306.1 GI:45824403
KEYWORDS
SOURCE Paracoccus marcusii
ORGANISM Paracoccus marcusii
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.

REFERENCE 1
AUTHORS Flachmann, R., Sauer, M., Schopfer, C.R., Klebsattel, M., Pfeiffer, A.M., Luck, T., and Voeste, D.
TITLE Use of a taxon-hin-containing plants or parts of plants of the genus tagetes as animal feed
JOURNAL Patent: WO 2004017749-A 9 04-MAR-2004
Sungene GmbH & Co. KGAA (DE); BASF Aktiengesellschaft (DE); BASF Plant Science GmbH (DE)
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ORIGIN
Query Match 95.8%; Score 698.6; DB 6; Length 729;
Best Local Similarity 97.4%; Pred. No. 3.3e-105;
Matches 720; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 ATGAGGCGACATGCTGCTGCCAAGGACGATTCAGCCGCACTGTTGCTGCGG 60
Db 1 ATGAGGCGACATGCTGCTGCCAAGGACGATTCAGCCGCACTGTTGCTGCGG 60
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Db 61 GGCATATGCGCGCGTGGCTGCGCTGATGTCATGCGTGGTGTTCGAGCGGGG 120
QY 121 GGCATATGCGCGCGTGGCTGCGGAAATTTCTGCGGCTGACCTGCTGCGGTCTG 180
Db 121 GGCATATGCGCGCGTGGCTGCGGAAATTTCTGCGGCTGACCTGCTGCGGTCTG 180
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QY 721 ACCGATGA 729
Db 721 ACCGATGA 729

RESULT 8
CQ793487 729 bp DNA linear PAT 29-MAR-2004
LOCUS CQ793487
DEFINITION Sequence 9 from Patent WO2004018693.
ACCESSION CQ793487
VERSION CQ793487.1 GI:45824578
KEYWORDS
SOURCE Paracoccus marcusii
ORGANISM Paracoccus marcusii
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Paracoccus.

REFERENCE 1
AUTHORS Schopfer, C.R., Flachmann, R., Herbers, K., Kunze, I., Sauer, M., and Klebsattel, M.
TITLE Method for the production of ketocarotenoids in flower petals on plants
JOURNAL Patent: WO 2004018693-A 9 04-MAR-2004
Sungene GmbH & Co. KGAA (DE)
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ORIGIN
Query Match 95.8%; Score 698.6; DB 6; Length 729;

Best Local Similarity 97.4%; Pred. No. 3.3e-105;
Matches 710; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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OY 721 ACCGCATGA 729
Db 721 ACCGCATGA 729
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RESULT 9
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DEFINITION Y15112
VERSION Y15112.1 GI:5912291
KEYWORDS asaxanthin biosynthesis; beta-carotene C-4 oxygenase; carotene hydroxylase; crtB gene; crtE gene; crtI gene; crtW gene; crtY gene; crtZ gene; geranylgeranyl pyrophosphate synthase; ketolase; lycopene beta-cyclase; phytoene desaturase; phytoene synthase.

SOURCE
ORGANISM Paracoccus marcusii
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteriaceae; Paracoccus.

REFERENCE
AUTHORS Harker, M. and Hirschberg, J.
TITLE Carotenoid biosynthesis genes in the bacterium Paracoccus marcusii

JOURNAL MHI
REFERENCE 2 (bases 1 to 6335)
AUTHORS Hirschberg, J.
TITLE Direct Submission
JOURNAL Submitted (12-SEP-1997) J. Hirschberg, The Hebrew Univ of Jerusalem, Dept of Genetics, Life Sciences Institute, Jerusalem 91904, ISRAEL

FEATURES

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ORIGIN

Query Match 95.8%; Score 698.6; DB 1; Length 6335;
Best Local Similarity 97.4%; Pred. No. 2e-105;
Matches 710; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
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QY 121 GCGCATCCATCTCGCGGCTCGGAATTTCTCGGGGCTGACCTGCTGCTGCTG 180
DB 529 GCCCATCCATCTCGCGGCTCGGAATTTCTCGGGGCTGACCTGCTGCTGCTG 588
QY 181 TTCATCATCGCGATGACGAGATGATGAGTGGTGGTGTGCTCCGCGGCGCGCGCAT 240
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DB 1129 ACCGATGATG 1137

RESULT 10
LOCUS CQ788335 729 bp DNA linear PAT 24-MAR-2004
DEFINITION Sequence 5 from Patent WO2004018695.
ACCESSION CQ788335
VERSION CQ788335.1 GI:45723102
KEYWORDS
SOURCE
ORGANISM Agrobacterium aurantiacum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
REFERENCE
AUTHORS Schopfer,C.R., Flachmann,R., Herbers,K., Kunze,I., Sauer,M. and
Klebsattel,M.
TITLE Method for producing ketocarotenoids in plant fruit
JOURNAL Patent: WO 2004018695-A 5 04-MAR-2004;
Sungene GmbH & Co. KGaA (DE)
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ORIGIN

Query Match 95.6%; Score 697; DB 6; Length 729;
Best Local Similarity 97.3%; Pred. No. 6.1e-105;
Matches 709; Conservative 0; Mismatches 20; Indels 0; Gaps 0;


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RESULT 12
LOCUS      CO793302              729 bp    DNA          linear    PAT 29-MAR-2004
DEFINITION Sequence 5 from Patent WO2004017749.
ACCESSION  CO793302
VERSION     CO793302.1   GI:45824399
KEYWORDS
SOURCE      Agrobacterium aurantiacum
ORGANISM    Agrobacterium aurantiacum
            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
            Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

REFERENCE
AUTHORS     1. Flachmann, R., Sauer, M., Schopfer, C.R., Klebsattel, M.,
            Pfeiffer, A.M., Luck, T. and Voeste, D.
TITLE        Use of astaxanthin-containing plants or parts of plants of the
            genus tagetes as animal feed
JOURNAL      Patent: WO 2004017749-A 5 04-MAR-2004;
            Sungene GmbH & Co. KGaA (DE); BASF Aktiengesellschaft (DE); BASF
            Plant Science GmbH (DE)
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ORIGIN
Query Match      95.6%; Score 697; DB 6; Length 729;
Best Local Similarity 97.3%; Pred. No. 6.1e-105;
Matches 709; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY 721 ACCGCAATGA 729
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DB 721 ACCGCAATGA 729

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DEFINITION Sequence 99 from Patent WO2004017749.
ACCESSION  CO793396
VERSION     CO793396.1   GI:45824493
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ORGANISM    Paracoccus sp. MBIC1143
            Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
            Rhodobacteraceae; Paracoccus.

REFERENCE
AUTHORS     1. Flachmann, R., Sauer, M., Schopfer, C.R., Klebsattel, M.,
            Pfeiffer, A.M., Luck, T. and Voeste, D.
TITLE        Use of astaxanthin-containing plants or parts of plants of the
            genus tagetes as animal feed
JOURNAL      Patent: WO 2004017749-A 99 04-MAR-2004;
            Sungene GmbH & Co. KGaA (DE); BASF Aktiengesellschaft (DE); BASF
            Plant Science GmbH (DE)
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Query Match      95.6%; Score 697; DB 6; Length 729;
Best Local Similarity 97.3%; Pred. No. 6.1e-105;
Matches 709; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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DB 61 GGCATATGCGCGCGTGGCTGCGCCCTGCGATGTCGATGCGCTGTTCGACGCGCG 120

QY 121 GCGCATCCCATCTCTGCGCGGTGCGGAATTTCTGCGGCTGACCTGCGTGTGCTGCG 180
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DB 121 GCGCATCCCATCTCTGCGCGGTGCGGAATTTCTGCGGCTGACCTGCGTGTGCTGCG 180

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REFERENCE 1
AUTHORS Schopfer, C.R., Flachmann, R., Herbers, K., Kunze, I., Sauer, M. and Klebatschel, M.
TITLE Method for the production of ketocarotenoids in flower petals on plants
JOURNAL Patent: WO 2004/018693-A 83 04-MAR-2004;
Sungene GmbH & Co. KGaA (DE)
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ORIGIN

Query Match 95.6%; Score 697; DB 6; Length 729;
Best Local Similarity 97.3%; Pred. No. 6.1e-105;

Matches 709; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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QY 721 ACCGATGA 729
DB 721 ACCGATGA 729
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Search completed: June 21, 2005, 22:57:51
Job time : 3379.93 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2005, 18:55:34 ; Search time 143.862 Seconds

(without alignments)
1359.734 Million cell updates/sec

Title: US-10-695-980-5

Perfect score: 1999

Sequence: 1 MSHDILLIAGAGLSGALIALA.....IPISQAVRCLPRPILQERA 382

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	795.5	39.8	382	Q47844	Q47844 pantocoe ags
6	783.5	39.2	382	O8GCS2	O8GCS2 pantocoe ste
7	782.5	39.1	386	O8VUJ6	O8VUJ6 pantocoe ags
8	779.5	39.0	385	O93C18	O93C18 xanthobacte
9	766.5	38.3	394	O9K1X3	O9K1X3 bradyrhizob
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11	671	33.6	391	O7M2F1	O7M2F1 photorhabdi
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13	551.5	27.6	434	O06756	O06756 erythrobact
14	195.5	9.8	501	LCYB_ARATH	O38933 arabidopsis
15	191.5	9.6	503	CCS_CITSI	O98640 citrus sine
16	187	9.4	490	O84V69	O84V69 zea mays (m
17	184.5	9.2	489	O6YUJ2	O6YUJ2 oryza sativ
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19	175.5	8.8	504	O64HC6	O64HC6 citrus sine
20	174.5	8.7	397	O82PA6	O82PA6 streptomyc
21	174.5	8.7	448	O93HP4	O93HP4 streptomyc
22	174.5	8.7	504	O8LPP7	O8LPP7 citrus sine
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27	172.5	8.6	504	O9MS46	O9MS46 citrus sine
28	170.5	8.5	498	LCYB_CAPAN	O43115 capsiu an
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ALIGNMENTS

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DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE Lycopene cyclase.			
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OS Flavobacterium sp. ATCC 21568.			
OC Bacteria; Bacteroidetes; Flavobacteriales;			
OC Flavobacteriaceae; Flavobacterium.			
OX NCBI_TaxID=50286;			
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RC STRAIN=R1534;			
RX MEDLINE=97186694; PubMed=9034310; DOI=10.1016/S0378-1119(96)00624-5;			
RA Pasamontes L., Hug D., Tessier M., Hohmann H.P., Schierle J.,			
van Loon A.P.;			
RT "Isolation and characterization of the carotenoid biosynthesis genes			
of Flavobacterium sp. strain R1534."			
RL Gene 185:35-41(1997).			
DR EMBL; U62808; AAC44851.1; "			
DR GO; GO:0045436; F:lycopene beta cyclase activity; IEA.			
DR GO; GO:0016705; F:oxidoreductase activity, acting on paired d. . .; IEA.			
DR CO; GO:0016117; P:carotenoid biosynthesis; IEA.			
DR InterPro; IPR010108; Carotene_cycl.			
DR Pfam; PF05897; CrcY; 1.			
DR TIGRFAMs; TIGR01790; carotene_cycl; 1.			
DR TIGRFAMs; TIGR01789; lycopene_cycl; 1.			
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Best Local Similarity	100.0%;	Pred. No. 1.1e-145;	
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DT 05-JUL-2004 (Rel. 44, Last annotation update)
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OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
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RX MEDLINE=96062243; PubMed=7592436;
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Ohtani T., Miki M.;
RT "Structure and functional analysis of a marine bacterial carotenoid
biosynthesis gene cluster and astaxanthin biosynthetic pathway
proposed at the gene level.";
RT J. Bacteriol. 177:6575-6584(1995).
RL -I- FUNCTION: Catalyzes the cyclization reaction which converts
lycopene to beta-carotene.
CC -I- PATHWAY: Carotenoid biosynthesis. Involved in astaxanthin
biosynthetic pathway.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@sib-sib.ch).
CC
DR EMBL, D58420; BAA09593.1; -.
DR InterPro; IPR010108; Carotene_cycl.
DR InterPro; IPR008461; Crty.
DR Pfam; PF05897; Crty; 1.
DR TIGRFAMs; TIGR01790; carotene_cycl; 1.
DR TIGRFAMs; TIGR01789; lycopene_cycl; 1.
KM Carotenoid biosynthesis.
SQ SEQUENCE 386 AA; 42202 MW; E14C41B688AFT78AC CRC64;

Query Match 72.8%; Score 1456; DB 1; Length 386;
Best Local Similarity 71.8%; Pred. No. 7.3e-104;
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Db 1 MTHDVLLAGAGLIALALRAAPDLRLVLLDHAAGPSDQHTWSCDPTDLSPEMLARL 60
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AC Q9RLH5;
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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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GN Name=crty;
OS Paracoccus marcusii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=59779;
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RP SEQUENCE FROM N.A.
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RA Harker M., Hirschberg J.;
RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: Y15112; CAB56061.1; -.
DR GO; GO:0045436; F:lycopene beta cyclase activity; IEA.
DR GO; GO:0016705; F:oxidoreductase activity, acting on paired d. . .; IEA.
DR GO; GO:0016117; P:carotenoid biosynthesis; IEA.
DR InterPro; IPR010108; Carotene_cycl.
DR InterPro; IPR008461; Crty.
DR Pfam; PF05897; Crty; 1.
DR TIGRFAMs; TIGR01790; carotene_cycl; 1.
DR TIGRFAMs; TIGR01789; lycopene_cycl; 1.
SQ SEQUENCE 386 AA; 42283 MW; 91952F0F33F36800 CRC64;

Query Match 70.3%; Score 1405; DB 2; Length 386;
Best Local Similarity 69.2%; Pred. No. 6.2e-100;
Matches 267; Conservative 43; Mismatches 72; Indels 4; Gaps 2;

Qy 1 MSHDLLIAGAGLIALAVRDRPDARIWMLDARSGPSDQHTWSCDPTDLSPEMLARL 60
Db 1 MTHDVLLAGAGLIALALRAAPDLRLVLLDHAAGPSDQHTWSCDPTDLSPEMLARL 60
Qy 61 SPIRGGEWTDQVAPPDHSRLTYGSGIEAGALIGLL--QGVDLRWNTHTVATLDDTGAT 118
Db 61 KPLRRANMPDQEVPRPHARRLATGYSIDGAALADAVRSGAETIRMSDIALDLDAQAT 120
Qy 119 LTDGSRIFAACVADARAVETPHLTVGFQKFGVEIETDAPAGVRRPMDATVPQMDGY 178
Db 121 LSCGRIEAGVLDGAGQAPSRHLTVGFQKFGVEIETDPRGVRPMDATVPQMDGY 180
Qy 179 RFIYLLPSPPTRIILIEDTRYSDGDLDDGALAQAASLDYVARRGWTGEMRRERGIPTAL 238
Db 181 GFIYLLPSPPTRIILIEDTRYSDGDLDDGALAQAASLDYVARRGWTGEMRRERGIPTAL 240
Qy 239 AHDAIGFRBHAQCAVAVGAGLGFHPTVGTSLPYAAQVADAIARBLTASARARAGMAI 296
Db 241 AHDAIGFRBHAQCAVAVGAGLGFHPTVGTSLPYAAQVADAIARBLTASARARAGMAI 300
Qy 297 GMAIDRADRDFRLNRLNRLFRGCPDRRYRLORFYRLPOPLIERFYAGRLTLADRLI 356
Db 301 DVAIDRADRDFRLNRLNRLFRGCPDRRYRLORFYRLPOPLIERFYAGRLTLADRLI 360

Db 363 SGKPPVLAALQAI 377

RESULT 6

08GCS2 PRELIMINARY; PRT; 382 AA.

AC 08GCS2; 01-MAR-2003 (TREMblrel. 23, Created)

DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DE Lycopene beta-cyclase.

GN Name=ctry;

OS Pantoea stewartii.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Pantoea.

OX NCBI_TaxID=66269;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 8200.

RA desouza M.L., Kollmann S.R., Schroeder W.A.;

RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY166713; AAN85598.1; -

DR GO; GO:0045436; F:lycopene beta cyclase activity; IEA.

DR GO; GO:0016705; F:oxidoreductase activity, acting on paired d. . .; IEA.

DR GO; GO:0016117; P:carotenoid biosynthesis; IEA.

DR InterPro; IPR010108; Carotene_cycl.

DR InterPro; IPR008461; Carotene_cycl.

DR Pfam; PF05897; Ctry; 1.

DR TIGRFAMs; TIGR01790; carotene-cycl; 1.

DR TIGRFAMs; TIGR01789; lycopene_cycl; 1.

SO SEQUENCE 382 AA; 43257 MW; 7893D4976C5FCCB1 CRC64;

Query Match 39.2%; Score 783.5; DB 2; Length 382;

Best Local Similarity 43.7%; Pred. No. 4.3e-52;

Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6;

QY 3 HDLIAGAGLGGALIALAVRDRRPARIWMLDARSGPSDQHTWCHDTLS--EWLAR 59

Db 5 YDLIVGAGLANGLIALRLQOQHPPMRILLIAGPEAGGNHTWSFHEEDLTINQHRWIA- 63

QY 60 LSPIRGEMTQEVAFPDHSRRLTTGYGSIAGALIGLIQ---GVDLRMNTHTVATLDDTG 116

Db 64 --PLVHHMPDYQVRFPQRRHVNSGYCVTSRHFAGILRQOFGHLMHTVSVVHMS 121

QY 117 ATLTDGSRIEACVIDARGAVETPHLTGFKFVGEIETDAPHGVERPMIMDATVPOMD 176

Db 122 VOLAGRIIHSSTVLDGRGYTPDSALRVGFQAFIQEWMQSLPHGLSEPIIMDAIVDQON 181

QY 177 GYRFYLLPFSPTRLIEDTRYSDGDLDDGALAQASLDVYARRGWTQGE--NRERGITLP 235

Db 182 GYRFYVYTLPLSATALLIEDTHYIDKANIQAERARONIRDYARQGMPLQTLIREQGLP 241

QY 236 IALAHDAIGFMRDHAOGAVPVGLGAGLFHPVTGSLPYAAQVADIAARDL--TTSASARA 294

Db 242 ITLVGDNRQFWMQOQPOAC--SGLRAGLFHPVTGSLPYALVALADRLSLADVTSSVHOT 299

QY 295 VRGMAIDRADRDRLFLRLINRMLFRGCPDPRRYRLIQRFYRLPOPLIEFVYAGRLTLADRL 354

Db 300 IAHFAGQWQOQGFRRMLNRMFLAAGPASPASRWVQRFGLPEDLIAFYAGKLVITDRL 359

QY 355 RIIVTGRPPIPLSQAVRCL 372

Db 360 RLISGKPPVPVLAALQAI 377

RESULT 7

08VU06 PRELIMINARY; PRT; 386 AA.

AC 08VU06; 01-MAR-2002 (TREMblrel. 20, Created)

DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DE Ctry protein.

GN Name=ctry;

OS Pantoea agglomerans pv. melleiae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Pantoea.

OX NCBI_TaxID=182454;

RN [1]

RP SEQUENCE FROM N.A.

RC Kamuntzen H., Hirata R.;

RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB076662; BAB79602.1; -

DR GO; GO:0045436; F:lycopene beta cyclase activity; IEA.

DR GO; GO:0016705; F:oxidoreductase activity, acting on paired d. . .; IEA.

DR GO; GO:0016117; P:carotenoid biosynthesis; IEA.

DR Pfam; PF05897; Ctry; 1.

DR TIGRFAMs; TIGR01790; carotene-cycl; 1.

DR TIGRFAMs; TIGR01789; lycopene_cycl; 1.

SO SEQUENCE 386 AA; 43674 MW; 1E7DB42C08447AE7 CRC64;

Query Match 39.1%; Score 782.5; DB 2; Length 386;

Best Local Similarity 43.8%; Pred. No. 5.2e-52;

Matches 168; Conservative 62; Mismatches 137; Indels 17; Gaps 8;

QY 3 HDLIAGAGLGGALIALAVRDRRPARIWMLDARSGPSDQHTWCHDTLS--EWLAR 59

Db 4 YDLIVGAGLANGLIALRLQOQPSLRILLIDAEREPANHTWSFHAEDLTETQHRWIA- 62

QY 60 LSPIRGEMTQEVAFPDHSRRLTTGYGSIAGALIGLIQ---GVDLRMNTHTVATLDDTG 116

Db 63 --PLVHHMPDYQVRFPQRRHVNSGYCVTSRHFAGILRQOFGHLMHTVSVVHMS 120

QY 117 ATLTDGSRIEACVIDARGAVETPHLTGFKFVGEIETDAPHGVERPMIMDATVPOMD 176

Db 121 VTLDDGRLTEDAVIDDGRGYQPDGALRMGFQSFQGEWQSLSEPHGLTAPIMDAIVDQQA 180

QY 177 GYRFYLLPFSPTRLIEDTRYSDGDLDDGALAQASLDVYARRGW--TGQEMRRRGITLP 235

Db 181 GYRFYVYTLPLSATALLIEDTHYIDNATLISGRARONIRDYARQGMPLQTLIREQGLP 240

QY 236 IALAHDAIGFMRDHAOGAVPVGLGAGLFHPVTGSLPYAAQVADIAARDL--TTSASARA 293

Db 241 ITLVGDVAAFPQNR---DLPCSLRAGLFHHTTGSLSPLAVALADRLAQMOTFSETLHA 297

QY 294 AVRGAIDRADRDRLFLRLINRMLFRGCPDPRRYRLIQRFYRLPOPLIEFVYAGRLTLADR 353

Db 298 TIQGFASQAOQOQFFRRMLNRMFLAAGPADQRMQVQRFGLPEDLIAFYAGKLVITDRL 357

QY 354 RIIVTGRPPIPLSQAVRCL--PER 375

Db 358 RLISGKPPVPVLAALQAIPTPHR 381

RESULT 8

093C18 PRELIMINARY; PRT; 385 AA.

AC 093C18; 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DE Lycopene cyclase.

GN Name=ctry;

OS Xanthobacter sp. (strain Py2).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Hyphomicrobiaceae; Xanthobacter.

OX NCBI_TaxID=78245;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Py2;

RA MEDLINE=22176293; PubMed=12189420;

RA Larsen R.A., Wilson M.M., Guse A.M., Metcalf W.W.;

RT "Genetic analysis of pigment biosynthesis in Xanthobacter autotrophicus Py2 using a new, highly efficient transposon mutagenesis system that is functional in a wide variety of bacteria.";

RL Arch. Microbiol. 178:193-201 (2002).

DR EMBL; AF408648; AAL01999.1; -.
DR GO; GO:0045436; F.lycopenene beta cyclase activity; IEA.
DR GO; GO:0016705; F.oxidoreductase activity, acting on paired d. .; IEA.
DR GO; GO:0016117; P.carotenoid biosynthesis; IEA.
DR InterPro; IPRO10108; Carotene_cycl.
DR InterPro; IPR008461; CrtY.
DR Pfam; PF05897; CrtY; 1.
DR TIGRfam; TIGR01789; carotene_cycl_1.
DR TIGRfam; TIGR01789; lycopenene_cycl_1.
SQ SEQUENCE 385 AA; 41442 MW; EFBC80BECE609FE CRC64;

Query Match 39.0%; Score 779.5; DB 2; Length 385;
Best Local Similarity 43.9%; Pred. No. 8,9e-52;
Matches 165; Conservative 58; Mismatches 148; Indels 5; Gaps 3

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Oy      4 DLLIAGLSGALIALAVRRPPDARIIMLDARSGPSDOHTWSCHDTDISPEWILARSPT 63
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      2 DIVFVGAGLANCLMAARIAAQRPGLHMLLEAGESVGNHSWSCSDSLTAAQAFLAPF 61
Oy      64 RRGETIDDEVAFPDHSRLRTTGYSIEACALISLLGG--VDLRNTHVALTDGTATLT 120
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      62 QSYLVAGGVHPAPSRTLKGGAYATISSERMEVNMERLCALRTVARVAHPDVHVE 121
Oy     121 DGSRIEACVIDARGAVERPHTLVGQKVGVAEITDPHGVRPMIMDATVQMONGYRF 180
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     122 GGERIDARAENVGRGPLASRHLDLYQTFLGOELRSRPGTLTPPLIMDAVQLGGYRF 181
Oy     181 IYLTFSPSTRILIETDRYSDGDLDGALAQSILDYAARGM-TGEEMRERRSIGLPALA 239
       :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     182 VYVLFLDDDTLLVEDTYVADGPDLPADLRGRISAIVAAQGMAVDVVREDEGLIPALG 241
Oy     240 HDAIFGMRDHAOGAAVPVGIAGLGIFHEVTGISLFPAAOADAIA-RDLTTASARRAVRW 258
       :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     242 GDINAFLETTPSGVAPAGRAGIFHFTPTGYSLPDAMALADSVALDLSGPAASAARSH 301
Oy     259 AIRADRDRFRFLANRMLEFGCGPPDRRYLLORFYVLPCQLIRFPYAGRLTLADRRIYT 358
       ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     302 AAAAANGKGFFPLLNNLMLEFRADPERRYAILORFYGLSIEDLIARFADRLTLTKAKRILS 361
Oy     359 GRPIPLSQAVRCLE 374
Db     362 GRPVSVRALSCLVE 377

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RESULT 9
09KIX3 ID 09KIX3 PRELIMINARY; PRT; 394 AA.

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AC    09KIX3          PROTEIN; NAME=PRELIMINARY;
BT    DT            OCT-2000 (TrEMBLrel. 15, Created)
DT    DT            OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI    DI            MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE    DE            Lycopenene cyclase.
GN    GN            Name=crtY;
OS    OS            Bradyrhizobium sp. ORS278.
OC    OC            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC    CC            Bradyrhizobiaceae; Bradyrhizobium.
OX    OX            NCBI_Taxid=114615;
RN    RN            [1]
RP    RP            SEQUENCE FROM N.A.
RC    RC            STRAIN=ORS278;
RX    RX            MEDLINE=20309720; PubMed=10851005;
RX    RX            DOI=10.1128/JB.182.J3.3850-3853.2000;
RA    RA            Hannibal L., Lorquin J., Angles d'Ortoli N., Garcia N.,
RA    Chaintreuil C., Masson-Bovivin C., Dreyfus B., Grand E.;
TI    TI            "Isolation and characterization of the canthaxanthin biosynthesis
RT    RT            genes from the photosynthetic bacterium Bradyrhizobium sp. strain
RT    RS278."
RL    RL            J. Bacteriol. 182:3850-3853(2000).
DR    DR            EMBL; AF218415; AAF78200.1; -.
DR    DR            GO; GO:0045436; F.lycopenene beta cyclase activity; IEA.
DR    DR            GO; GO:0016705; F.oxidoreductase activity, acting on paired d. .; IEA.
DR    DR            GO; GO:0016117; P.carotenoid biosynthesis; IEA.
DR    DR            GO; GO:0006118; P.electon transport; IEA.

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DR InterPro: IPR010108; Carotene_cycl.
DR InterPro: IPR008461; Crty.
DR InterPro: IPR000172; GMC_oxred.
DR Pfam; PF05897; Crty; 1.
DR Pfam; PF0732; GMC_oxred N; 1.
DR TIGRFAMs; TIGR01790; carotene-cycl; 1.
DR TIGRFAMs; TIGR01789; lycopene cycl; 1.
DR SEQUENCE 394 AA; 43435 MW; 8BDDDD59304EB194A CRC64;

Query Match 38.3%; Score 766.5; DB 2; Length 394;
Best Local Similarity 44.0%; Pred. No. 9.2e-51;
Matches 172; Conservative 56; Mismatches 134; Indels 29; Gaps 9;

QY 4 DLIANGSGSLIALAVDRRPPARIVMLDARSGSDQHTWSCHDPLDSE---TLARL 60
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 6 DVIYGGGLAGCLIALRLTARPDRLVILIEGSSISIGNHTWSFFGDISSDQAMICRL 65
QY 61 SPIRGWTDQEVAFPHSRRLTGYGSIIEAGLIGLIGQVDLDMNTHV-----ATL 112
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 66 VGNR---WPGEVFAFHAIRLIRLSTAYLSMTS---TLRAVEQGFPERILRDATATISAT 119
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 113 DDTGATLTDSRIEACVVIDARCAVETPHLTVGQFQVGEIETDAPGVPRMIMDATV 172
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 120 DH--VVLGGRTLAFPCVIDARGGRPVGLATGRQKLTGLEVRLLAAPHGLDVPIMDATV 177
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 173 PQNDGRTFYLLPSPFRILLIEDTRYSDGDLDDGALAQASLDVLAARGWTGQG-MRRER 231
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 178 AOSGGEYFVYVTLDPDPRLLIEDTVYSDGGLPEQVLAQRVARALAKGQIAEIRAEQ 237
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 232 GIIPDIALAHAIQFWRDHAGQAVVGLGAGLHFHVTGYSLPYAAQVADAIAR-----DL 286
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 238 GVLPVILAGDSGL-VSKPDSPPRVGLAALLVHFTTGYSLPDAVKAVDDLTLARLAQKAL 296
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 287 TTASARBAVAGWADIRADRDRFLRLNRMLEFRGCPDPRRYRLQRFYRLPQPLIERFYAG 346
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 297 SSADARFTIDCYGTTIRRRGGYVFLNRMLEFKAAPEBERRHILARFFGLDQALIERFYAA 356
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 347 RLTLADRLRI---VTGRPPILPLSQAVCLPE 374
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 357 RIQPDKLRVFMHMLMKRPPIPSISALCLPE 387
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 10
CRTY_ERHME STANDARD; PRT; 386 AA.
AC 001331;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lycopene cyclase.
GN Name=crty;
OS Erwinia herbicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pantoea.
OX NCBI_TaxID=549;
OX [1]
RC SEQUENCE FROM N.A.
RC STRAIN=Ehno10;
RX MEDLINE=93138098; PubMed=8422926; DOI=10.1016/0014-5793(93)81188-6;
RA Hundle B.S., O'Brien D.A., Beyer P., Kleinig H., Hearst J.E.;
RT "In vitro expression and activity of lycopene cyclase and beta-
RT carotene hydroxylase from Erwinia herbicola.";
RL FEBS Lett. 315:329-334(1993).
CC -1- FUNCTION: Catalyzes the cyclization reaction which converts
CC lycopene to beta-carotene.
CC -1- PATHWAY: Carotenoid biosynthesis.
CC -----
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CC EMBL; M87280; AAA64980.1; -.
 CC PIR; S52981; S52981.
 DR InterPro; IPR010108; Carotene_cycl.
 DR InterPro; IPR008461; CrtY.
 DR Pfam; PF05897; CrtY; 1.
 DR TIGRFAMs; TIGR01790; carotene_cycl; 1.
 DR TIGRFAMs; TIGR01789; lycopen_cycl; 1.
 KW Carotenoid biosynthesis.
 SQ SEQUENCE 366 AA; 43341 MW; F4A40563BFCFA980 CRC64;

Query Match 37.5%; Score 750; DB 1; Length 386;
 Best Local Similarity 43.0%; Pred. No. 1.7e-49;
 Matches 166; Conservative 51; Mismatches 149; Indels 20; Gaps 6;

QY 4 DLLIAGAGLGGALIALAVRRRPPARIYMLDARGSPSOQHTWSCHDITLSPWMLARLSP 63
 DB 3 DLLIVGGGLANGILAMRQRQYPOINLLITEGEGPGGNHTWSFHEDDLTPGQHMIALPL 62
 QY 64 RRGWTDQEVAPDPDSRLTTGSGIEAGALIGLQ---GVDLRNNTVATLDDTGTATLT 120
 DB 63 VAHMPGVEVQPPDLRRRLARGYVITSRRFAALHQAIGENIWCNCSVETLPSVRLA 122
 QY 121 DGSRIEACVIDARGAVETPHLTGFGKFGVGEIETDAPHGERMINDATVPQMDGYRF 180
 DB 123 NGEALLAGAVIDRGVITASAMQGYQLFGQOMRLTOPHGLTVPLINDATVAQGGYRF 182
 QY 181 IYLLPFSPRLILIEDTRYSDGDDLDGALAQSILDYAARGW-TGQEMRRERGLPIALA 239
 DB 183 VYTLPLSADTLIEDTRYANVPORDNALRQTVTVYAHSKWQLALEREETGCLPITLA 242
 QY 240 HDAIFWMDHAGAVPVGAGLFPHTVGYSLPYAAOVADALIA---ARDLTASARR 293
 DB 243 GDIOALMD-AGVRSRSGRAGLPHFTTGYSLPLVALADALADSPRLGVSVLGYLTQGF 301
 QY 294 AVRGALIDRADRFRLINRLFRGCCPDRRYLLQRFYRLPOPILIEFYAGRLTLADR 353
 DB 302 AERHNR-----RQGFRLINRLFLAGREERNRVMQRFYGLPEPTVERFYAGRLSLPDK 356
 QY 354 LRIYGRPPILPSQAVRC---LPER 375
 DB 357 ARLTGKPPVPLGEAMRAALNHPDR 382

RESULT 11

Q7MZFL PRELIMINARY; PRT; 391 AA.

AC Q7MZFL; 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE CrtY protein.
 GN Name=CrtY; OrderedLocustNames=plu4341;
 OS Photorhabdus luminescens (subsp. launondii);
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photorhabdus.
 NC NCBI_TaxID=141679;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TT01;
 RX MEDLINE=22957627; PubMed=14528314;
 RA Duchaud E., Rusanlok C., Frangoul L., Buchrieser C., Givaudan A.,
 RA Teourt S., Bocs S., Boursaux-Bude C., Chandler M., Charles J.-F.,
 RA Daaba E., Derose R., Derzelle S., Freyssiuet G., Gaudriault S.,
 RA Medigue C., Lanois A., Powell K., Sigstier P., Vincent R., Wingate V.,
 RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
 RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
 luminescens.";
 RT Nat. Biotechnol. 21:1307-1313(2003).
 RL EMBL; BX571873; CAE16713.1; -.
 DR PhotoList; plu4341; -.
 DR GO; GO:0045436; F:lycopene beta cyclase activity; IEA.

DR GO; GO:0016705; F:oxidoreductase activity, acting on paired d. . .; IEA.
 DR GO; GO:0016117; P:carotenoid biosynthesis; IEA.
 DR InterPro; IPR010108; Carotene_cycl.
 DR InterPro; IPR008461; CrtY.
 DR Pfam; PF05897; CrtY; 1.
 DR TIGRFAMs; TIGR01790; carotene_cycl; 1.
 DR TIGRFAMs; TIGR01789; lycopen_cycl; 1.
 KW Complete proteome.
 SQ SEQUENCE 391 AA; 44725 MW; 240ECC992E10B21P CRC64;

Query Match 33.6%; Score 671; DB 2; Length 391;
 Best Local Similarity 41.0%; Pred. No. 2e-43;
 Matches 155; Conservative 57; Mismatches 152; Indels 14; Gaps 8;

QY 4 DLLIAGAGLGGALIALAVRRRPPARIYMLDARGSPSOQHTWSCHDITLSP---EWLRL 60
 DB 6 DLLIVGGGLANGILAMRQCKPHRLVLLINTERIGNHTWSFHQDLTGAHEHMIAPL 65
 QY 61 SPIRGWTDQEVAPDPDSRLTTGSGIEAGALIGLQ---GVDLRNNTVATLDDTGTGA 117
 DB 66 IYR---WSGYDVIFPAFQRTLPHSYFISITQHPASIIHAYIGERIQLRLVQELTPQKV 122
 QY 118 TLTGSRLEACVIDARGAVETPHLTGFGKFGVGEIETDAPHGERMINDATVPQMDG 177
 DB 123 YLQDSSLSAGAVIDRGMRPGPIGSGTQAFQGEWLESHTLPIIMDTSGQDTG 182
 QY 178 YRFIYLPFSPRLILIEDTRYSDGDDLDGALAASL-DYARRGW-TGQEMRRERGLP 235
 DB 183 YRFIYLPFSSRLILIEDTHVDRGP-PDKLSQATIAEVAKKGWKGLIRESSGLP 241
 QY 236 IALAHDAIGFRDHAQAVPVGAGLFPHTVGYSLPYAAOVADALIA-RDLTTASARRA 294
 DB 242 ITLNDFTSFPAQLA-GQPTGLRALFHPHTTGYSLPHAILARIVALLPELDTSLFIT 300
 QY 295 VRGALIDRADRFRLINRLFRGCCPDRRYLLQRFYRLPOPILIEFYAGRLTLADR 354
 DB 301 LRDVARDQMRQRFRLINRLFLAGDPQGRVQWRFYSLPNLIARFVABOLNSVDKA 360
 QY 355 RIYVGRPPILPSQAVRCL 372
 DB 361 RILICKPPVPIKGLAKAM 378

RESULT 12

O6MMA6 PRELIMINARY; PRT; 379 AA.

AC O6MMA6; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Lycopene cyclase.
 GN OrderedLocustNames=Bd1730;
 OS Bdellovibrio bacteriovorus.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
 OC Bacteriia; Proteobacteriia; Bdellovibrio.
 NC NCBI_TaxID=959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RX PubMed=14752164; DOI=10.1126/science.1093027;
 RA Rendulic S., Jagtap P., Rosinus A., Bpinger M., Baar C., Lanz C.,
 RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
 RA Sockett R.E., Schuster S.C.;
 RT "A predator unmasked: 11fe cycle of Bdellovibrio bacteriovorus from a
 genomic perspective.";
 RT Science 303:689-692(2004).
 RL EMBL; BX842650; CAE79599.1; -.
 DR GO; GO:0045436; F:lycopene beta cyclase activity; IEA.
 DR GO; GO:0016705; F:oxidoreductase activity, acting on paired d. . .; IEA.
 DR GO; GO:0016117; P:carotenoid biosynthesis; IEA.
 DR InterPro; IPR010108; Carotene_cycl.
 DR InterPro; IPR008461; CrtY.
 DR Pfam; PF05897; CrtY; 1.

DR TIGRFAMs: TIGR01790; carotene-cycl, 1.
 DR TIGRFAMs: TIGR01789; lycopene_cycl, 1.
 KW Complete proteome.
 SQ SEQUENCE 379 AA; 42420 MW; 1A3F7D98A512A54 CRC64;

Query Match 32.4%; Score 648.5; DB 2; Length 379;
 Best Local Similarity 37.4%; Pred. No. 1.1e-41;
 Matches 144; Conservative 70; Mismatches 138; Indels 33; Gaps 9;

QY 4 DLIAGAGSGALIALAIVDRRDPARIWMDARSGSDQHTWSCHDTLSPF--WLAKLS 61
 DB 11 DCLIVGGGAGGILLQALRTQPELKVLLERGTQGGNHTWSFHGSDVPGATWQSLI 70
 QY 62 PIRGEMTDQEVAFPHDSRLTTGYSIEA---GALIGLQGVDRMNTHTVATLDDTGA 117
 DB 71 ---SKTPAYEVRFPYKOKIOSSYSIKADPHQKLLG-QHSQILLQASVQEVARDV 126
 QY 118 TLTDGSRIBACVVDARGAVERPHLTVGQKVEVEIETDAPHGERPMIMATVPQMDG 177
 DB 127 TLDDGMFPAKCVIDARGMGAADVAKRGYQKFGVLVYKLSOPHGLNHTVILKDLVLPQVDG 186
 QY 178 YRFYTLPPSPRILIEDTRYSDGDLDDGALAQAASLDYPAARRGW-TGQEMRERGIPTI 236
 DB 187 YRFYVTLPPWSETELLVEDTYSTNTPLDYATLKSGLIDYIAGKWTESVITRQEVGCLPL 246
 QY 237 ALAHDAIGFWRDHAQAVPVGIGA--GLPHPTVGSGLPYAAQVADAIARDLTTASARRA 294
 DB 247 DLYDVAV---EGSGSGPLNAGASGVQPVGTGYFPQTAVCAVQALASSLDT----- 296
 QY 295 VEGWA-----IDRADRDRLALNRMFLRGCPDRRYLLQRFYRLPQPLIERFYAGR 347
 DB 297 ---MGSVLPALQNTNYKKQARLYRLINRMFLAAVPEKRYVILLERFLLSEALIERFYQGR 353
 QY 348 LTLADRLRIVTGRPPILPSQAVRCL 372
 DB 354 LTVLDQVRILCGKPPVSVNRALKSL 378

RESULT 13

ID 006756 PRELIMINARY; PRT; 434 AA.
 AC 006756;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Lycopene cyclase.
 GN Name=crty;
 OS Erythrobacter longus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
 OC Sphingomonadaceae; Erythrobacter.
 OK NCBI_TaxId=1044;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=och 101;
 RX MEDLINE=97311406; PubMed=9168123; DOI=10.1016/S0378-1119(96)00788-3;
 RA Matsumura H., Takayama H., Hasekabe E., Burgess J.G., Matsumura T.,
 RT "Cloning, sequencing and expression the carotenoid biosynthesi genes,
 RT lycopene cyclase and phytoene desaturase, from the aerobic
 RT photosynthetic bacterium Erythrobacter longus sp. strain Och 101 in
 RT Escherichia coli.";
 RT Gene 189:169-174(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=och 101;
 RA matsumura h., hasekabe e., matsumura t.,
 RX EMBL: D83513; BAA20275.1; -;
 DR GO: GO:0045436; F:lycopene beta cyclase activity; IEA.
 DR GO: GO:0016705; F:oxidoreductase activity; acting on paired d. .; IEA.
 DR GO: GO:0016117; P:carotenoid biosynthesis; IEA.
 DR InterPro: IPR010108; Carotene_cycl.
 DR Pfam: PF008461; Crty, 1.

DR TIGRFAMs: TIGR01790; carotene-cycl, 1.
 DR TIGRFAMs: TIGR01789; lycopene_cycl, 1.
 KW Complete proteome.
 SQ SEQUENCE 434 AA; 48018 MW; 9E440E09BA5AEF47 CRC64;

Query Match 27.6%; Score 551.5; DB 2; Length 434;
 Best Local Similarity 36.0%; Pred. No. 3.7e-34;
 Matches 142; Conservative 55; Mismatches 164; Indels 33; Gaps 10;

QY 2 SHDLIAGAGSGALIALAIVDRRDPARIWMDARSGSDQHTWSCHDTLSPF--WLAKLS 61
 DB 14 SCDCALVGGGAGGILLQALRTQPELKVLLERGTQGGNHTWSFHGSDVPGATWQSLI 73
 QY 62 PIRGEMTDQEVAFPHDSRLTTGYSIEA---GALIGLQGVDRMNTHTVATLDDTGA 115
 DB 74 DFRQIDMEGVEYRFPKRYKLTAVRSWASVDFHGLLRALPEGSVILGRKAVG-LDAR 132
 QY 116 GATLT---DGRIBACVVDARGAVERPHLTVGQKVEVEIETDAPHGERPMIMATVPQMDG 170
 DB 133 GVDLAPSQYGPATRIARSVIDCRSEKPSAHKGGQVFLGHHMRLOEBPHGVENPIMDA 192
 QY 171 TVPQM-----DGYRITVLLPPSPRILIEDTRYSDGDLDDGALAQAASLDYPAARRGW-T 223
 DB 193 TVDQALPHNGSGSYRPPVYVPLGSHDVFIEDTYADPLLDNNALSGRIDYARANGWEN 252
 QY 224 GQEMRERGIPLIALAHDAIGFWRDHAQ--GAVPGLAGLPHPTVGSGLPYAAQVADAI 281
 DB 253 GTPVHHEAGVLPVLTGCD-FSAVQDEVRLPGVAILAGARGFTPHPLSTYMCVAVERALAM 311
 QY 282 A-----ARDLTASARRAVRGMAIDRADRDRLALNRMFLRGCPDRRYLLQRFYRL 335
 DB 312 ASQPDLSGSQLAAPFDSRRARRMS-----KTGYRLRLARFLFAAPEKRYVILLERFLLSEALIERFYQGR 366
 QY 336 PQLIERFYAGRLTLADRLRIVTGRPPILPSQAV 369
 DB 367 REGILIERFYAARSNTFDKRVLMGEPVAIHSAI 400

RESULT 14

ID LCVB_ARATH STANDARD; PRT; 501 AA.
 AC Q38933; Q39145;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Lycopene beta cyclase, chloroplast precursor (EC 1.14.-.-).
 GN Name=LCY1; Synonyms=LYC; OrderedLocustNames=Ac3g10230;
 GN ORFNames=F14P13.17;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsie.
 OK NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=96434545; PubMed=8837512;
 RA Cunningham F.X., Jr., Fosson B., Sun Z., McDonald K.A., Dellapenna D.,
 RA Gantt E.;
 RT "Functional analysis of the beta and epsilon lycopene cyclase enzymes
 RT of Arabidopsis reveals a mechanism for control of cyclic carotenoid
 RT formation.";
 RT Plant Cell 8:1613-1626(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wassilewskija;
 RA Scolnik P.A., Bartley G.B.;
 RT "Nucleotide sequence of lycopene cyclase from Arabidopsis.";
 RL (er) Plant Gene Register PGR95-019.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Giuliano G., Rosati C., Santangelo G.;
 RT "Gene structure and regulation of the carotenoid biosynthesis pathway
 RT in Arabidopsis thaliana.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cnv. Columbia:
 RX MEDLINE=21016720; PubMed=1130713; DOI=10.1038/35048706;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unselid M.,
 RA Fattmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delaeny M., Boutry M., Griveil L.A., Mache R., Pulgdenesch P.,
 RA De Simone V., Cholme N., Artiguenave F., Robert C., Broctier P.,
 RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Muebach E., Drzozek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionaci B.,
 RA Conrad A., Hoenischer K., Kauer G., Loehner T.-H., Nordstiek G.,
 RA Reichelt J., Schaefer M., Schoen O., Barques M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottewillder B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Lilauro C., Purnelle B., Masny D.,
 RA de Haan M., Maare A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argitlou A., Flores M., Iignori R., Vitale D.,
 RA Mannheim G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T.H., Rizzo M., Walts R., Wu D., Peterson J., Van Aken S.,
 RA Creasy T.H., Haas B., Malt R., Gall J.E., Feldlyum T.V.,
 RA Pal G., Miltcher J., Sellers P., Gall J.E., Feldlyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Preiser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Ideawa K., Kawashina K., Ishida Y.,
 RA Kiyokawa C., Kohara M., Matsuno M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yaeuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana."
 RL Nature 408:820-822(2000).
 CC -1- FUNCTION: Catalyzes the double cyclization reaction which converts
 CC lycopene to beta-carotene and neurosporene to beta-zeacarotene.
 CC -1- PATHWAY: Carotenoid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- SIMILARITY: Belongs to the lycopene cyclase family.
 CC
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 CC -----
 CC EMBL, U50739; AAB53337.1; -;
 CC EMBL, L40176; AAB81880.1; -;
 CC EMBL, AF117256; AAF82388.1; -;
 CC EMBL, AC009400; AAF02819.1; -;
 CC InterPro: IPR010108; Carotene_cycl.
 CC InterPro: IPR008671; Lycopene_cycl.
 CC InterPro: IPR00205; NAD_BS.
 CC Pfam: PF05834; Lycopene_cycl; 1.
 CC TIGFAMS: TIGR01790; carotene_cycl; 1.
 CC Carotenoid biosynthesis; Chloroplast; NAD; Oxidoreductase;
 KW Transit peptide.
 FT CHAIN 1 80 Chloroplast (Potential).
 FT NP BIND 85 501 Lycopene beta cyclase.
 FT FT BIND 85 113 NAD (Potential).
 FT CONFLICT 31 31 NAD (Potential).
 FT CONFLICT 243 243 V -> I (in Ref. 2).
 FT CONFLICT 243 243 V -> I (in Ref. 2).
 SQ SEQUENCE 501 AA; 56176 MW; C3014578DBD4E2 CRC64;
 Query Match 9.8%; Score 195.5; DB 1; Length 501;
 Best Local Similarity 23.4%; Pred. No. 1.1e-06;
 Matches 111; Conservative 66; Mismatches 144; Indels 153; Gaps 27;
 Oy 4 DLIAGAGSGLTILALVDRPRDARIWLDARSGPSDQHTSCHDITLSPFWLARLSP 63
 Db 84 DLATVGGPAGLAIVAOVSE--AGLSVCSID--PSPRLTW-----PN 121

Oy 64 RRGWTDQ-----EVAPDH--SRRLTGYGSIAGALIG-----LLQ 99
 Db 122 NYGVWVDEFEAMDLLDCIDTTWSGAVVYVDEGVKDLSPYGRVNRKQLEKSMLOKCTTN 181
 Oy 100 GVDLAKN--TIVATLDTGAL--TDGSRIFAACYIADRG-----AVETHLVYPRKF 149
 Db 182 GVKFQSKVTNVH--EENNSTVSCSDGVKIDASVLDATGFSRCLVQYDKY--NGYQVA 239
 Oy 150 VGVLEIETA--PHGVRPIMATVPOMDGY-----RFIYLPSPFRLIEDPT 197
 Db 240 YGIAVAVDGHFPDDKVPFMDWRKHLDYELKERNSKIPTFLYAMFSSNRIFLEET- 298
 Oy 198 YSDGDDLDGALQASL-----DYARRCWYQEMRR-----ERGLIPALAHDAIGFW 246
 Db 299 -----SLVAPGLMEDIOERMARLKHGLINVGRIEDEDVCVIMG----- 340
 Oy 247 RDHAGANP-----VGLG--AGLEFHPVGY-----SLPYAQQVADALARLTASARRA 294
 Db 341 -----GPLPVLPRVVGIGTAGWVHPSTGYVARTTAAAPIVANAI--VRLGSPSS--NS 393
 Oy 295 VRG-----WAIDRADRFRLRLNMLFRGCPDPRRYLLQRFYRLPQPLIERF 343
 Db 394 LRQGLSAEWRDMPIRERRQREFRCGMQILK-IDLDATRRFDFAPFDLQPHYMGF 452
 Oy 344 YAGRLTLAD-----RLRVTGRPPIPSQAVRCIPERPLIOER 381
 Db 453 LSSRLFLPBLVFGSLFSPHSANSTRLEIMT-KGVPLAKMI-----NNLVQDR 500
 RESULT 15
 CCS_CITSI
 ID CCS_CITSI STANDARD, PRT, 503 AA.
 AC Q9SEAO;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Capsanthin/capsorubin synthase, chloroplast precursor.
 GN Name=CCS;
 OS Citrus sinensis (Sweet orange).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eusteroles II; Sapindales; Rutaceae; Citrus.
 OX NCBI_TaxID=27111;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xu C.J., Chen D.M., Zhang S.L.;
 RT "Molecular cloning of capsanthin/capsorubin synthase gene from orange
 (Citrus sinensis)."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Catalyzes the conversion of the ubiquitous 5,6-
 CC epoxycarotenoids, antheraxanthin and violaxanthin, into capsanthin
 CC and capsorubin, respectively.
 CC -1- PATHWAY: Carotenoid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Chloroplast; chromoplast (by similarity).
 CC -1- SIMILARITY: Belongs to the lycopene cyclase family.
 CC
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 CC
 CC -----
 CC EMBL, AF169241; AAF18389.1; -;
 CC InterPro: IPR010108; Carotene_cycl.
 CC InterPro: IPR008671; Lycopene_cycl.
 CC Pfam: PF05834; Lycopene_cycl; 1.
 CC TIGFAMS: TIGR01790; carotene_cycl; 1.
 CC Carotenoid biosynthesis; Chloroplast; NAD; Oxidoreductase;
 KW Transit peptide.
 FT TRANSIT 1 ? Chloroplast (Potential).

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OM protein - protein search, using sw model

Run on: June 17, 2005, 19:18:35 ; Search time 33.0577 Seconds

(without alignments)
111.838 Million cell updates/sec

Title: US-10-695-980-5

Perfect score: 1999
Sequence: 1 MSHDLLIAGAGLGGALIALA.....IFLSQAVRCLPRLPLQGERA 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	810.5	40.5	382	2 C37802	crty protein - Erw
2	795.5	39.8	382	2 S52585	dycopene cyclase -
3	750	37.5	386	2 S52981	lycopene cyclase -
4	162	8.1	410	2 D75475	lycopene cyclase -
5	161.5	8.1	500	2 S66350	lycopene beta-cycl
6	161.5	8.1	500	2 S72505	lycopene beta-cycl
7	161	8.1	500	2 S72506	lycopene beta-cycl
8	160	8.0	500	2 S66349	lycopene beta-cycl
9	155	7.8	405	2 T37022	probable lycopene
10	132	6.6	498	2 S71511	capsanthin/capsoru
11	126.5	6.3	526	2 T07082	lycopene epsilon-c
12	125	6.3	408	2 D70549	hypothetical prote
13	122	6.1	402	2 AC2797	hypothetical prote
14	122	6.1	402	2 C97576	2-octaprenyl-6-met
15	117	5.9	388	2 T36402	probable monooxyge
16	116	5.8	338	2 C70553	hypothetical prote
17	115.5	5.8	421	2 E97689	hypothetical prote
18	115.5	5.8	421	2 AB2915	FAD-dependent mono
19	114.5	5.7	377	2 D87483	ribonucleotide red
20	114	5.7	508	2 S44950	lmbc protein - Str
21	112.5	5.6	466	2 C83407	hypothetical prote
22	112.5	5.6	471	2 S51511	capsanthin/capsoru
23	111.5	5.6	1021	2 H75423	hypothetical prote
24	111	5.6	391	2 G85566	hypothetical prote
25	111	5.6	406	2 T36632	probable oxidoredu
26	109.5	5.5	456	2 D84202	hypothetical prote
27	109	5.5	391	2 AD0584	probable monooxyge
28	109	5.5	412	2 A83461	hypothetical prote
29	108.5	5.4	1542	2 AC3173	conjugal transfer

30	108	5.4	391	2 D90716	oxygenase [importe
31	108	5.4	429	2 AH3272	2-octaprenyl-3-met
32	108	5.4	757	2 JC7726	(1->4)-alpha-D-glu
33	107	5.4	398	2 G82755	conserved hypothet
34	106	5.3	610	2 T06280	probable starch sy
35	105.5	5.3	408	2 H87193	probable FAD-likke
36	105.5	5.3	429	2 F84015	maltose/maltodextr
37	105	5.3	337	2 D87354	conserved hypothet
38	105	5.3	391	2 D64801	probable monooxyge
39	104.5	5.2	476	2 T36395	probable transcrip
40	104	5.2	475	2 T35799	probable oxidoredu
41	104	5.2	503	2 S55589	D-nopaline dehydro
42	104	5.2	549	2 JC7158	steroid monooxygen
43	103.5	5.2	392	2 AG0873	2-octaprenyl-6-met
44	103.5	5.2	472	2 AC0863	l-fuculose kinase
45	103	5.2	433	2 H87660	peptidoglycan-bind

ALIGNMENTS

RESULT 1

C37802
crty protein - Erwina uredovora
C/Species: Erwina uredovora
C/Date: 31-May-1991 #sequence_revision 31-May-1991 #lexc_change 09-Jul-2004
C/Accession: C37802
R/Misawa, N.; Nakagawa, M.; Kobayashi, K.; Yamano, S.; Izawa, Y.; Nakamura, K.; Harashio, J. Bacteriol. 172, 6704-6712, 1990
A/Title: Elucidation of the Erwina uredovora carotenoid biosynthetic pathway by funcitc
A/Reference number: A37802; PMID:91072214; PMID:2254247
A/Accession: C37802
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-382 <MIS>
A/Cross-references: UNIPROT:P21687; GB:D90087; NID:9216681; PIDN:BA14126.1; PID:9216684
C/Superfamily: Erwina dycopene cyclase

Query Match 40.5%; Score 810.5; DB 2; Length 382;
Best Local Similarity 45.6%; Pred. No. 3.5e-56;

Matches 171; Conservative 59; Mismatches 138; Indels 7; Gaps 4;

QY	3	HDLLIAGAGLGGALIALAVDRRPARIVMLDARGSPDQHTWSCCHDTLSPEMLARLSR	62
DB	5	YDLILVAGLGLNLRLQOOQPMKRIILIDAPAGGNHTWSTFHDDLTSSQHRWIP	64
QY	63	IRRGWTDGEVAFPPHSRLTTGYGIEAGLIGLQ--GVDLRNTHVATLDTGTATL	119
DB	65	LVVHHWPDYQVAFPTRRRLNGSGYFCITSGRPAEVLQRFQPHLWMDTVAEVAESVRL	124
QY	120	TGGSRIEACVTDAGAVETPHLTVGQFQVEVEIETDAPHGVERPMIMDATVPMQDGR	179
DB	125	KKGQVIGARAVIDGRYAANSALSVGFQIQERLSPHGLISSFTINDATVDDQNGR	184
QY	180	FYLLPFPSPTRILIEDTRYSDGDDLDGALAASLDYARRGMTQGE-WRRRGILPIL	238
DB	185	FYVSLPSTRLILIEDTHYIDNATIDPECARONICDYAAQOGWQOTLIREGALPITL	244
QY	239	AHDAIGFWRDHAQAVPVGAGLPFPVTGSLPYAAQVADAIARDL-TTASARRAVRG	297
DB	245	SGNADAFWQORPLAC--SGLRAGLFPTTGYSLPLAVAVADRLSALDVFSTSIHHAIR	302
QY	298	VAIDRADRPRLNLNRMIFRCGPDRRRLRLQRFRLPOPILERYAARLTALRLRTV	357
DB	303	FAERWQOGFPRMNRMLFLAGPADSRWRVQRFYGLPEDLIRAYAKLTITLRLITL	362
QY	358	TGRPPIPLSQAVRCL 372	
DB	363	SGKPPVPVLAALQAI 377	
RESULT 2			
			S52585

dDyocope cycylase - Erwinia herbicola
C:Species: Erwinia herbicola
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S52585
R:Lin, Y.P.; Lai, E.M.; To, K.Y.; Chang, Y.S.; Liu, S.T.
Mol. Gen. Genet. 245, 417-423, 1994
A:Title: Transcriptional activation of flanking sequences by Tn1000 insertion.
A:Reference number: S52583, MUID:95107237, PMID:7806390
A:Accession: S52583
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-382 <Lin>
A:Cross-references: UNIPROT:O47844; EMBL:M90698; NID:G14893; PIDN:AAA21262.1; PID:G14893
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1992
C:Superfamily: Erwinia dyocope cycylase

	Query Match	39.8%;	Score 795.5;	DB 2;	Length 382;
	Best Local Similarity	44.3%;	Pred. No. 5.2e-55;		
	Matches	166;	Conservative	64;	Mismatches 138; Indels 7; Gaps 4;
QY	3	HDLIAGAGLSGALIALAVDRDRPDARIWMLDABSGPSDDHTWSCHDTLSPENMLARISP	62		
Db	5	YDLILVIGANGNLGIATLRLOOQPDMRILLIEAARQAAGNCTNSFHDADLTIESORHWAP	64		
QY	63	IRRGEMTDQEVAFPDHSRLTGTGGSIEAGALLGLQ--GVDLRMNHVTLLTDGTALT	119		
Db	65	LVTWHPEYQVRPFPRRRKLNSGFPSVTSQRPAEVLQOKFGQHLMISANAVEHADAVRL	124		
QY	120	TDSRIEAAACYIDARGAVETPHLTITVGQKFGEVLEIETDPHGEVERPMIMATAVPQMONGYR	179		
Db	125	NNGOVISASNAVVDGGYTPNSALNVGFQAFIQGEWRLLSKPHGLSPIIMDAITVDQQNGYR	184		
QY	180	FYLPLPSEPTKILLIEDTRYSDGGDIIDGALAQAOSLDIYAARGWTGQE-MREERGTLPLAL	238		
Db	185	FVYSPLPSATELILEDTHYIDNATLEPERARONTRDVAACQDWOLQLTLREEGCALPYTL	244		
QY	239	AHDAIGFERDHAGAANPVYGLGAGLFHPVTGYSLPYPAAOVADAIAARDL-TASARRAVRG	297		
Db	245	TGDSTAFMQO--QPLACSGLRAGLFHPFTTGISLPYLAVALMRLSMDVFTSSIHQAITH	302		
QY	298	WAIDRADRDFRLRLNRMLFRGCCPDRERYLLQRFYRLPOBLIRFYAGRLLTADRIRIV	357		
Db	303	FAHERMOQOQFFRMLNRMLFLAGPADSRMWRVMORYGLPEDLISRFAYGKLTLDRLIRIL	362		
QY	358	TGRPPILPSQAVRCL	372		
Db	363	SGKEPVPVTAALQAI	377		

RESULT 3
S52981
lycopenene cyclase - *Erwinia herbicola*
C:Species: *Erwinia herbicola*
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S52981
R:Hundel, B.; Alberti, M.; Niewelstein, V.; Beyer, P.; Kleinig, H.; Armstrong, G.A.; Bun
Mol. Gen. Genet. 245, 406-416, 1994
A:Title: Functional assignment of *Erwinia herbicola* Eho 10 carotenoid genes expressed in
A:Reference number: S52976; MUID:95107236; PMID:7808389
A:Accession: S52981
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-386 <HUN>
A:Cross-references: UNIPROT:001331; EMBL:M87280; NID:q148404; P1DN:AAA64980.1; PID:q1484
C:Genetics:
A:Start codon: GTG
A:Superfamily: *Erwinia* dycopenene cyclase

Query Match 37.5%; Score 750; DB 2; Length 386;
 Best Local Similarity 43.0%; Pred. No. 2e-51;
 Matches 166; Conservative 51; Mismatches 145; Indels 20; Gaps 6;
 4 DLIAGAGLSCALILAVRDRRPPARIYMLARSGSPSQTWWSCHDITLSPEMLARLSPI 63

Db 3 DLILVGGILNGLIMWRLRQYRPLNMLLEAGHQPGQGNHTWGFHEDDLRPGQHNIAWPL 62
QY 64 RRGWTDQEVAFRPHSRRLTTGYSIEAGALLGLQ---GVDLRMNTHVATLDDTGATLT 120
Db 63 VAHMPGEYQFQPLRLRRRLARGYYSITSERFAEALHQAIGENIWLWNSVEELPNSVRLA 122
QY 121 DGSRIEACVADARGAVETPHLTWGFQKPFVGEIETDAPHGVERPMIMDAITVQMDGYRF 180
Db 123 NGEMLLAGAVIDGGVYASSAMQGYQLFQCGQMRLLTQPHGLVYPLIMDITVQAQCGSYRF 182
QY 181 IYLLPSPFRLIEDTRYSDGGIDLDGALAQAASLDIYARRGW-TGQEMRRERGILPLALA 239
Db 183 VYTLPLSADTLTIEDTRYANVPQRDDNALQVTLVDYASHSGWOLAQDERETGCLPTTLA 242
QY 240 HDAIGPRDHQAQVAPVGLAGLPHRPVYGSPLPAAQVANAIA-----ARDLTTSARR 293
Db 243 GDIALMAD-APGVPRSGMRAGLFHPFTGYSLEPLAVNALMADISDPRLGSVPLXQLTRQF 301
QY 294 AVRGMAIDRADRDRFLNRLMRLERGCPPDRRYRLQRFYRLPQPLIERFYAGLTLADR 353
Db 302 AERHMR-----RQFFFLNRLMLFLAGRENRMRVMQRFYGLDEPPTVERFYAGLSLFDK 356
QY 354 LRIYGRPPPLPSQVRC-----LPER 375
Db 357 ARILTGKRPVPLGEAMRPAALNHPPDR 382

RESULT 4
D75475
Lycopene cyclase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
A:Accession: D75475
R:White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M., Shen, M.; Vamshaveyan, J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75475
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-410 <WHI>
A:Cross-references: UNIPROT:Q9RW68; GB:AE001934; GB:AB000513; NID:56458504; PIDN:AAF1037
A:Experimental source: Strain R1
C:Genetics:
A:Gene: DR0801
A:Map position: 1

[illegible]

252 -GAVPVGLGAGLPHPTVGYSLPYAAQVAAIAARDLTTASAR---RAVGMAI-----DR 302
 261 GGVLAVGAAGAAVHPVSGVQVAGALSDAAGVATA-IATLLCGCKDAAMAAALNSPERK 319
 303 ADRREPLRLNMLFRGCPDRRRLRLQFYLRLPQLIERFY-----AGRLTLADRLRIV 357
 320 AARE--VHLGVGALLGLBRALPHFPGFFGLPFGROMARFLHPTDAGTLA-RTWLRVF 376
 358 T---GRPPIPLSQAVRCLP 373
 377 AQTGRVRLPLARMAAQAQ 395

RESULT 5

S66350
 Lycopen beta-cyclase (EC 5.5.1.-) - tomato
 C:Species: Lycopersicon esculentum (tomato)
 C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 28-Jul-2000
 C:Accession: S66350
 R:Pecker, I.; Gabbay, R.; Cunningham Jr., F.X.; Hirschberg, J.
 Plant Mol. Biol. 30, 807-819, 1996
 A>Title: Cloning and characterization of the cDNA for lycopen beta-cyclase from tomato
 A:Reference number: S66349; M01D:96194462; PMID:8624411
 A:Accession: S66350
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-500 <PE>
 A:Cross-references: EMBL:X86452
 C:Superfamily: tomato lycopen beta-cyclase
 C:Keywords: intramolecular lyase; isomerase

Query Match 8.1%; Score 161.5; DB 2; Length 500;
 Best Local Similarity 21.7%; Pred. No. 5.1e-05;
 Matches 103; Conservative 70; Mismatches 146; Indels 155; Gaps 28;
 4 DLLIAGAGLGAIIA-----LAVDRRPPARIWMLDARSGPSDQHTW-----S 46
 85 DLAVVGGGAGLAVAAQVSEAGLSVCSIDPNFKLIW-----PNNYGVWVDFEAMDLID 138
 47 CHDTLSPEWMLARLSPIRGEWTDQVAFPDHSRR-LTTGYGSIKAGALIG-----LLQ 99
 139 CLD-----ATWGAAYVIDMTAKDLHRYGRVNRKQKSKMOKCINM 182
 100 GVDLRKNTHTVATLDDTGATL---TDGSRLEACVLDARG-----AVETPHLTVGQKRV 150
 183 GVKFHQAKVIKVIHESKSMILCNDGITITQATVVDATGFSRLVQYDPRY-NPGYQVAY 241
 151 GV--ELETDAIPHVERPMIMD-----ATVPQMDGYRFTYLLPFSPTRL 192
 242 GILAEVE-EHPFDVNMKVMMDRDSHLKNTDLKERNRIIP-----TFLYANPFSSNRIF 295
 193 IEDTRY--SDGGDLDDGALAQAQLDYAARRGWTQEMRR-----ERGILPILAHDAIGFW 246
 296 LEETSIVARPGRLRID--IQERM--VARLNHGIKIVKSIIEDEHCLIPMG----- 341
 247 RHAQAVP-----VGLG--AGLPHPTVGY---SLPYAAQVADAI-----AAR 284
 342 -----GRLPVLDPORVVGIGTAGMVPSPGYWARTLAAPVANAIIQYLGSESHSGN 396
 285 DLTTASARRAVGMAMD-RADRDREFRLNMLFRGCPDRRRLRLQFYLRLPQLIERF 343
 397 ELSTAVWKUL---WPIERRRQREFFCGMDILKLDLPATRRF--FDAFEDLEPRYWHGF 451
 344 YAGRLTLAD-----RLRIVTGRPPILSQAVRCLPERPLQER 381
 452 LSSRLFLPELIVFGSLFSHASNTSRFEIMT-KGTVPLVNMI-----NNLLQDK 499

RESULT 6
 S72505
 Lycopen beta-cyclase (EC 5.5.1.-) - tomato
 C:Species: Lycopersicon esculentum (tomato)

C>Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 09-Jul-2004
 C:Accession: S72505
 R:Pecker, I.; Gabbay, R.; Cunningham Jr., F.X.; Hirschberg, J.
 submitted to the EMBL Data Library, April 1995
 A>Description: Cloning and characterization of the lycopen cyclase gene from tomato.
 A:Reference number: S72505
 A:Accession: S72505
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-500 <PE>
 A:Cross-references: UNIPROT:Q43503; EMBL:X86452; NID:g1006672; PID:g1006673
 C:Superfamily: tomato lycopen beta-cyclase
 C:Keywords: intramolecular lyase; isomerase

Query Match 8.1%; Score 161.5; DB 2; Length 500;
 Best Local Similarity 21.7%; Pred. No. 5.1e-05;
 Matches 103; Conservative 70; Mismatches 146; Indels 155; Gaps 28;
 4 DLLIAGAGLGAIIA-----LAVDRRPPARIWMLDARSGPSDQHTW-----S 46
 85 DLAVVGGGAGLAVAAQVSEAGLSVCSIDPNFKLIW-----PNNYGVWVDFEAMDLID 138
 47 CHDTLSPEWMLARLSPIRGEWTDQVAFPDHSRR-LTTGYGSIKAGALIG-----LLQ 99
 139 CLD-----ATWGAAYVIDMTAKDLHRYGRVNRKQKSKMOKCINM 182
 100 GVDLRKNTHTVATLDDTGATL---TDGSRLEACVLDARG-----AVETPHLTVGQKRV 150
 183 GVKFHQAKVIKVIHESKSMILCNDGITITQATVVDATGFSRLVQYDPRY-NPGYQVAY 241
 151 GV--ELETDAIPHVERPMIMD-----ATVPQMDGYRFTYLLPFSPTRL 192
 242 GILAEVE-EHPFDVNMKVMMDRDSHLKNTDLKERNRIIP-----TFLYANPFSSNRIF 295
 193 IEDTRY--SDGGDLDDGALAQAQLDYAARRGWTQEMRR-----ERGILPILAHDAIGFW 246
 296 LEETSIVARPGRLRID--IQERM--VARLNHGIKIVKSIIEDEHCLIPMG----- 341
 247 RHAQAVP-----VGLG--AGLPHPTVGY---SLPYAAQVADAI-----AAR 284
 342 -----GRLPVLDPORVVGIGTAGMVPSPGYWARTLAAPVANAIIQYLGSESHSGN 396
 285 DLTTASARRAVGMAMD-RADRDREFRLNMLFRGCPDRRRLRLQFYLRLPQLIERF 343
 397 ELSTAVWKUL---WPIERRRQREFFCGMDILKLDLPATRRF--FDAFEDLEPRYWHGF 451
 344 YAGRLTLAD-----RLRIVTGRPPILSQAVRCLPERPLQER 381
 452 LSSRLFLPELIVFGSLFSHASNTSRFEIMT-KGTVPLVNMI-----NNLLQDK 499

RESULT 7

S72506
 Lycopen beta-cyclase (EC 5.5.1.-) - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C>Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 09-Jul-2004
 C:Accession: S72506
 R:Pecker, I.; Gabbay, R.; Cunningham Jr., F.X.; Hirschberg, J.
 submitted to the EMBL Data Library, September 1994
 A>Description: Cloning and characterization of the lycopen cyclase gene from tomato.
 A:Reference number: S72506
 A:Accession: S72506
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-500 <PE>
 A:Cross-references: UNIPROT:Q43578; EMBL:X81787; NID:g1006689; PID:g1006690
 C:Superfamily: tomato lycopen beta-cyclase
 C:Keywords: intramolecular lyase; isomerase

Query Match 8.1%; Score 161; DB 2; Length 500;
 Best Local Similarity 22.7%; Pred. No. 5.6e-05;
 Matches 105; Conservative 62; Mismatches 151; Indels 144; Gaps 27;

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OY      4  DLLTAGAGLSGLILAAVRDRPPARIVWLDRSGSPQOHTSGCHDTLSPEWLARLSPI 63
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      85  DLAVVGGGPGGLAAQOYSE--AGLSVSIID--PSEKLIY-----PN 122
OY      64  RRGEXTDQ-----EVARPDH--SRRLTGYGSIAGALIG-----LIQ 99
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      123  NYGVVWDFEFAEMDLDCLDATWSGTVVYIDDTWTKDLDRPYGRVNRKQJSKRMQKILIN 182
OY      100  GVDLRKNTHTVATLDDTGATL--TDGSRLEACVUIDAG-----AVETPHLTGPFQKTV 150
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      183  GYKPFHAKVIKIVHEAKSMILCNDGVTTIQATVVLADGFSKCLVQYDQPY-KPGQVAY 241
OY      151  GV--EITDAPHPGVPRMIMD-----ATVPQMDGGRFYIYLLPFSPTIL 192
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      242  GLIAEVE--EHPDTSKMYLMDRDSHLGNMELKERNKRV-----TPIYANPFSNKIF 295
OY      193  IEDTRY--SDGGLDDGALAQAQLDYAARGTGTQEMRR---ERGILPITALHADIQFW 246
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      296  LEETSLVARPGILRMD--IQERM--VALNLHGIKVSIEEDECVIIPMG----- 341
OY      247  RDHQAQAVP-----VGLG--AGLFHPVYGY--SLPVAQVNAAI--AARDLTTA 289
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      342  ----GSLPVLTPQRVVGTGTAGLVHPSTGYVAVARTLAAAPVANAALIIHYLQSEKOLCAN 396
OY      290  SARRAVRG--VAID--RADRDREFLRLNLNLFPGCPDREYRLLOFYRLPOPLIERFYAG 346
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      397  ELAAVWMDLWPIERRQREFFCFQGMILLKULDLATRFRF--FDAFPDLERPYWHGFLSS 454
OY      347  RLTLAD-----RLAIYGRPIPIPSQAVRCL 372
        |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      455  RLVIPELIFPGSLFSPRASNTSRIEIMT-KGTLPLVNMIMNL 495

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Db      296 LEETSLVAPGRLRDD---IOERM--VARLNHGIIKKSIEEDENHCVIPMG----- 341
Oy      247 RDHQGVNP-----VGLG--AGLEHPVTGY----SLPYAAQVADAI-----AARDLTTA 289
Db      342 -----GSLPYIPQRYVGTGTAGLVHPSTGIMVARTAAAPVANAIIHLYSEKDLGN 336
Oy      290 SARBAVNG--WAID--RADRDRLFLNLNMLFRGCPDRRYRLLOFYRLPOPLIERPYAG 346
Db      397 ELAAVWKDLPIPIRRRRQREFPCGMIDLKLDLPAATRR--PDAPFDLEPRYWHGFLSS 454
Oy      347 RLTLAD-----RLRIYGRPRPLSGAVCL 372
Db      455 RLYPELPIFGSLSPRASNTSRLEIWT-KGTLPVMMINNL 495

RESULT 9
T37022
probable lycopen cyclase - Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Date: 03-Dec-1999 #sequence #revision 03-Dec-1999 #text_change 09-Jul-2004
C.Accession: T37022
R.Murphy, L.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A.Reference number: Z21619
A.Accession: T37022
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1405 <MR>
A.Cross-References: UNIPROT:Q9RI55, EMBL:AL099899, PIDD:CAM53415.1, GSPDB:GN00070, SCOPED
A.Experimental Source: Strain A3(2)
C:Genetics:
A:Gene: crty; SCOPDB:SCU12.03c

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RESULT 8
S66349
lycogene beta-cyclase (EC 5.5.1.-) - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 28-Jul-2000
C:Accession: S66349
Ripecker, I.; Gabbay, R.; Cunningham Jr., F.X.; Hirschberg, J.
Plant Mol. Biol. 30, 807-819, 1996
A>Title: Cloning and characterization of the cDNA for lycogene beta-cyclase from tomato
A:Reference number: S66349; MUID:96194462; PMID:8624411
A:Accession: S66349
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-500 <PEC>
A:Cross-references: EMBL:X81787
C:Superfamily: tomato lycogene beta-cyclase
C:Keywords: intramolecular lyase; isomerase

Query Match      8.0%; Score 160; DB 2; Length 500;
Best Local Similarity 22.5%; Pred. No. 6.7e+05;
Matches 104; Conservative 62; Mismatches 152; Indels 144; Gaps 26;

OY    4 DILLGAGISGLTALAVRRPRDARIWLDARSGPSDOHTSCHDTLSPEWLRLSTI 63
      |||::||::||::||::||::||::||::||::||::||::||::||::||
DB    85 DLVAVGGPAGIAVAQOVSE--AGLSVSID-----PSPKLIW-----PN 122
      |||::||::||::||::||::||::||::||::||::||::||::||::||

OY    64 RRGEMTDQEVAF-----PDHSRLITGVGSIEAGALIG-----LLQ 99
      |||::||::||::||::||::||::||::||::||::||::||::||::||
DB   123 NYGVAVNDEEPAADLLDCLDATWSGVVVYIDDNTTKDLDPYGRVNRKKQSKSMOKCIIN 182
      |||::||::||::||::||::||::||::||::||::||::||::||::||
OY   100 GVVDLRMNTIVATLDDTGATL---TDGSRLEACVIDARG-----AVETPHLTVGSGKEV 150
      |||::||::||::||::||::||::||::||::||::||::||::||::||
DB   183 GVKFHAKVIKIYIHBEASMLICNDGVTIQATLVLDATGFSKCLVOYDKPY-KPGYQAVY 241
      |||::||::||::||::||::||::||::||::||::||::||::||::||

OY   151 GV-VLETDAFPGVERPMIMD-----ATVPQMDSGYRFYYLLFPSPTRLI 192
      |||::||::||::||::||::||::||::||::||::||::||::||::||
DB   242 GLIAVEV-EHPDPTSDMVLDWRDSLGNMELKERNRKV-----TLFYAMPFGSNKIF 295
      |||::||::||::||::||::||::||::||::||::||::||::||::||

OY   193 IEDTRY--SDGDLDLGALQAQLDYAAARGMTQGEMR-----ERCILFIALAHLAIGFW 246
      |||::||::||::||::||::||::||::||::||::||::||::||::||

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Query Match          7.8%; Score 155; DB 2; Length 405;
Best Local Similarity 22.9%; Pred. No. 0.0013;
Matches 105; Conservative 45; Mismatches 155; Indels 154; Gaps 23;

QY      DLLIAGISGALTAIAVDRRPPARIIVMLDARSGP--SDQHTWSCHDTLSDEMTARLS 61
       |||::||::||::||::||::||::||::||::||::||::||::||::||:
DB      DVLIIGGAALSLAHNLTEGTAPAMTIVPEPPGLRPARRTW-CY----- 55
QY      62 PIRRGWTDGEVAPRDHSRLTTGYGSI EAGALI GLIQVDLRNT--HVA----TL D 113
       |         |||::||::||::||::||::||::||::||::||::||::||:
DB      56 -----W-----GAADGLEAVGASWSVLRLHGADGGSVTV D 87
QY      114 DTGATL-----TDGSRI-----EAC----- 129
DB      88 PAPFTYRWVSADPERWHGRLTARDGARILKRTAESVRVAPGTEVRTCLPGGRPLTY 147
QY      130 ---YTDAKGAEFPHL-TVGFQKEVG---VELETDA--PHGVPRMIMDATVPQ-MDG YRF 180
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB      148 ARRVFDSPLDELPPARCCLQHFRGMFWVTTRIDREPRAVAD--LMDFPVPQAHGLAF 204
QY      181 IYLFPSPTRLIEDTRYSDG---GDLDGGLAQASILDYAARGWTGOENRRERGLPIA 237
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB      205 GYVLPFLADRLVITYTERSRAPLTTEAYESALGHYCND ILGLSELYVE- RTQGVIPMT 262
QY      238 LAHAIDIGFWHDQAQAV-PVGLGAGLFHPVYTGSYLPAQAVADAIAA--RD---LTTAS 290
       :         |||::|||::|||::|||::|||::|||::|||::|||::|||:
DB      263 DAR-----PCGRAPRAYVYRIGTAGCATRPATGYFAVAQSHSGATAIALDHGHRVPAPH 317
QY      291 AARA-----VRGMAIDRADRDREFLLRLNRMLFRGCPDRRRRYLLORFRLRQPLIERF 343
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB      318 GRRARAMDAAVILRALDITGRIDGPRPFPTDL-----FRVPAERLLRF 358
QY      344 YAGRLTTLADRILYITGRPPIPLSQAVCLPERPLQERA 382
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
DB      359 LDGTTSLREEWGIGLRTFVRPM--LRTAAEVPLPRRS 394

RESULT 10
S71511
capsanthin/capsorubin synthase (EC 5.5.1.-) - pepper

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N:Alternate names: chromoplast-specific protein
N:Contents: capsorubin synthase; capsanthin synthase
C:Species: Capsicum annuum (pepper)
C:Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
C:Accession: S71511; J02141
R:Bouvier, F.; Hugueney, P.; d'Harlingue, A.; Kuntz, M.; Camara, B.
Plant J. 6, 45-54, 1994
A>Title: Xanthophyll biosynthesis in chromoplasts: isolation and molecular cloning of an
A:Reference number: S71511; MUID:9504653; PMID:7920703
A:Accession: S71511
A:Molecule type: mRNA
A:Residues: 1-498 <BOU>
A:Cross-references: UNIPROT:Q42435; EMBL:X76165; NID:9522119; PIDN:CAAS3759.1; PID:9522119
A:Experimental source: cv. Yolo wonder
R:Devereux, J.; Bouvier, F.; Steppuhn, J.; Klein, A.; Camara, B.; Kuntz, M.
Biochem. Biophys. Res. Commun. 199, 1144-1150, 1994
A>Title: Structure and expression of two plant genes encoding chromoplast-specific protease
A:Reference number: JC2140; MUID:94197697; PMID:8147854
A:Accession: JC2141
A:Molecule type: DNA
A:Residues: 1-498 <DEB>
A:Cross-references: EMBL:X77289; NID:9468747; PIDN:CAAS4495.1; PID:9468748
A:Experimental source: cv. Yolo wonder
R:Devereux, J.; Bouvier, F.; Steppuhn, J.; Klein, A.; Camara, B.; Kuntz, M.
Biochem. Biophys. Res. Commun. 201, 466, 1994
A:Reference number: A55775
A:Contents: annotation; erratum
A>Note: The legends of the nucleotide sequence figures were reversed in publication (see
A:Genetics:
A:Gene: CCS
A:Complex: monomer
C:Function:
A>Description: catalyses the conversion of the ubiquitous 5,6-epoxycatenoids, antheraxa
A:Pathway: carotenoid biosynthesis
C:Superfamily: tomato lycopen beta-cyclase
C:Keywords: chromoplast; intramolecular lyase; isomerase

Query Match 6.6% Score 132; DB 2; Length 498;
Best Local Similarity 19.6%; Pred. No. 0.011;
Matches 89; Conservative 68; Mismatches 154; Indels 144; Gaps 20;

Db 4 DLIAGAGLSGALIALAVDRPDAIYMLDARSGPSDOHTWSCHDTDLSPEWLARLSP I 63
 :::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
 83 DVIIIGTPAG--LRLAQVSKYGIKVCVD-----PPLSLMW-----PN 120

Db 64 RRGEXTOE-----VAEPDH-SRRLTGGTGSIEAGAL-TGLIQG-VDL 103

Db 121 NYGVWVDFEFKLGEDCLDHKWPSCVHISDHKTXYLDPRPYGRVSRKKLKLLNSCVEN 180

Oy 104 RMNHVATL-----DDTGATLVDSGRLEAACVIDANG-----AVETPLTVTFQKFV 150

Db 181 RVKFIKAVLKYKHIEFFSSIVCDGKRKISGLVLVDASGYASDIETDKPR-NHGVOVAH 239

Oy 151 GVRIETD-APGVERPMID-----ATVPOMDYRFYLPPSPTRILLIEDTRY 198
 :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 240 GILAEVDNDHPDLLDMWRSHLGNBPRLRVKNTEPEPTFLAMPDRDLVLEE-- 297

Oy 199 SDGDVLDGALAQAQLDV-----AARGMTGQEMR---REGKILPALAHAIQFMR 247
 :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 298 -----SLYSRPMLSMEVKRRMVALRHGIKRVSLVEEKCVTIMGSPLPRI---- 345

Oy 248 DHAGAVPVGGAAGLFHPVTGSLPYAAOVADAIAARLTVAASRAVRAGWAIDRADRD 307

Db 346 --PQNVAIGGTSGIVHPSGGYMAKSMAALPVLAALVESLGSTMIRG----- 393

Oy 308 FLRLINRMFLFGCCPDNR-----YLLORFYRLPOLIERFYAG 346
 :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 394 -SOLYHRVMNGMLPESDRVRRECYCFGMETLLKLDELSTRTLLPAFPVDVDPKWMGFSS 452

Oy 347 RLTLAD-----RLRIYGRPIPI 365
 :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 453 RLSVKEELAVLSLYLFGHASNLARDITV-KCTVPL 486

RESULT 11

T07082

Lycopene epoxidase-cyclase (EC 5.5.1.-) - tomato

C1Species: Lycopodium esculentum (tomato)

C1Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C1Accession: T07082

R1Cohen, G.; Cohen, M.; Zamir, D.; Hirschberg, J.

submitted to the EMBL Data Library, July 1997

A1Description: Regulation of expression of the gene for lycopene epoxidase cyclase during

A1Reference number: Z15905

A1Accession: T07082

A1Status: preliminary; translated from GB/EMBL/DBJ

A1Molecule type: mRNA

A1Residues: 1-526 <R0N>

A1Cross-references: UNIPROT:O65837; EMBL:Y14387; NID:e1285211; P1DN:CAA74745.1; P1D:e128

A1Experimental source: Cultivar VF36; leaf

C1Genetics:

A1Gene: CrtL-e-1

A1Map position: 12

C1Function:

A1Description: converts lycopene to delta-carotene

C1Superfamily: tomato lycopene beta-cyclase

C1Keywords: intramolecular lyase; isomerase

Query Match 6.3%; Score 126.5; DB 2; Length 526;

Best Local Similarity 21.1%; Pred. No. 0.011;

Matches 89; Conservative 55; Mismatches 164; Indels 113; Gaps 20;

QY 4 DLIAAGLGLSALIALVDRRRPPARIYMLDASGP-----SDQHTSCHDITLSPFWLA 58

DB 107 DLVIVGGCPAG--LATAASAKGLNVGLV-----GPDLPFTNNYGVNDEPKDGLG----- 155

QY 59 RLSPIRGEMTDGEVAFPPDSRLTTG--YG-----SIEAGALIGLQGV 102

DB 156 -LQACIEHWMD-TIVVLDDDEPILIGRAGRSRHLHEELKRCYEAQVL----- 205

QY 103 LRWHTVAITLDDTGATLTDGSR1---EAACVTDAR-----GAVETPHL-----TVGF 146

DB 206 -----YLNKSKYDR1VEATNGSLVECGDVV1PCRFVTVASGAASGKFLQYELGSPRVSV 260

QY 147 QKTVGEIETD-APHGVERPMINDATVPQMDGTR-----FYILLPSPT 189

DB 261 QTAGVEEVEVDNPNFDESLWFM-----YRDYLHDAOSLEAKYPTFLYMPMSP 312

QY 190 RILIEDPRYSDGGLDDGALAQSLDYAARGWTCGEMRER-GILPITALHDAIGFWRD 248

DB 313 RVFEETCLASKDMPPDLKKIKMLRLNTLVGRIKELIYBEMSYIVG-----GSLPN 366

QY 249 HAQAVPVGAGLGFHVTGY---SLPYAAQVADA-----ARDLTASARRAVRG 297

DB 367 TEQNTLAFGAASVHVAHATGVSVRSLSEAPKCAVLANILRHYSKMLTSSSIPST 426

QY 298 -----WALDRADDFRLRLNMLFRGCPDRRRLYLQRFYLPQPLIERFFYAGRLTLA 351

DB 427 QAWNTLWPOER-KRQSFPLFGALILQLDIEGRSFFRAFFRVKMMWGFLGSSLSA 485

QY 352 D 352

DB 486 D 486

RESULT 12

D70549

hypothetical protein Rv0561c - Mycobacterium tuberculosis (strain H37Rv)

C1Species: Mycobacterium tuberculosis

C1Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C1Accession: D70549

R1Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtrold, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A1Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

Job time : 36.0577 secs

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QY 145 GE-----QKFGVEIETDAPHG-----VERPMINDATVPOMDG 177
DB 170 GIGVXSWSPQTAVVLTNFSHRPHGVSTEFHTPTGPFQVPLPDDRSSLVWVTPQ-- 227
QY 178 YRFVLLPSPFRILLIEDTRYSDGDDLDGALAQAASLDYAARRGWTGQEMRRER-GILPI 236
DB 228 ABELTALPLETTLAKVEEWMQSMLGAVTENSVOA-----WPLSMTAHRFGKGRV 278
QY 237 ALAHDAIGFWRDHAQAVVGLGAGLFHVTGYSLEPYAAQVADATTAARDLTTASARRAVR 296
DB 279 ALIGEA-----AHGFPPIG-----AQGLNT-----SLRDITALTTELGAVSDRPIA 319
QY 297 GWAIDRADRDREFLRNLNMLFRGCPDRRRYRLQRFYRLPQPLIERFYAGRLTIADRLRI 356
DB 320 ADAGSSFDKRRADYVSRLL-----SYDLINR-----SLISDFLPQWARRAGLHV 365
QY 357 VTG-----RPPILSQAVRCLP 373
DB 366 LSGIGTLRSMVMREGIEPGRGLKALP 391
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RESULT 15

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T36402
probable monoxygenase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T36402
R:Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21606
A:Accession: T36402
A:Status: preliminary; translated from GB/EMBL/DDBL
A:molecule type: DNA
A:Residues: 1-368 <SAU>
A:Cross-references: UNIPROT:Q9RK22; EMBL:AL109974; PDB:1AB53314.1; GSPDB:GN00070; SCOPED
A:Experimental source: strain A3(2)
C:Genetic8:
A:Gene: SCOEDB:SCF34.03c
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Query Match 5.9%; Score 117; DB 2; Length 388;

Best Local Similarity 23.4%; Pred. No. 0.12;

Matches 92; Conservative 52; Mismatches 132; Indels 118; Gaps 22;

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QY 7 TAGAGISGL-----IALAVRRRPARIVMLDARSGEDQ-----TWSCHDTDS 53
DB 13 IIGAGGGJLTCAVLRHGLAVTVYDRDPA--ASRDQGSIDLHEBDGQLAREAGLL 69
QY 54 PEMLARLSPIRGEWTDQEVAFPDHSRL-----TTGYGSIEAGALIG--LLQGV-- 102
DB 70 EEFPA-----LARGE-SQERRRFTACRLGRLLPDEGETARPEIDRGQLRGILLIESLDAG 124
QY 103 -LRMNTHTVATLDDTG-----ATLTDSRIEACVIDARGAV-----TPHLT-VGF 146
DB 125 TVRMWGLSIVSGPAPGPRTLFTDGSIVETDLVIGDGAFSRVRAAVSDAVPRYTVGF 184
QY 147 QKFGVEIETDAPHGVEPMINDATVPQMDGYRFIY-----LIPFSPTRIIEDTRY 198
DB 185 LEAMFDMESAHPHELSE--LVGRSAHVADGGQLPAQRNSGGMRYVWRRAVAL--DMWT 241
QY 199 SDG--GDLDGALAQASLDYAARRGWTGQEMRR-----ERGITPITALAHDAIGFWR 247
DB 242 ASGLRPDDTDGIRARLLAEYA--GMSPTRLRMITENDGYVDRPLPALPVPHY-----WR 294
QY 248 -----DHAQAVPVGIGAGLFHPTGYSLEPYAAQVADATTAARDLTTASARRAVR-- 296
DB 295 PTPGVTLTGDAHLMPLGIVNL-----AMLDGAELALALAA-----SATVDAVRY 343
QY 297 -----GWAIDRADRDREFLR 311
DB 344 EKTMLPRSAEIAIGMLEGAGFLLEBPDAEDLRL 377
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Search completed: June 17, 2005, 19:38:04

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2005, 19:37:17 ; Search time 130.394 Seconds
(without alignments)
1124.898 Million cell updates/sec

Title: US-10-695-980-5

Perfect score: 1999

Sequence: 1 MSHDLIAGAGLSCALIALA.....FLSQAVCLPERPLQERA 382

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1999	100.0	382	9	US-09-547-267-7
2	1999	100.0	382	10	US-09-920-923-5
3	1999	100.0	382	15	US-10-695-980-5
4	783.5	39.2	382	10	US-09-941-947A-10
5	783.5	39.2	382	14	US-10-218-118-6
6	783.5	39.2	382	15	US-10-363-567-30
7	783.5	39.2	382	15	US-10-466-656-4
8	783.5	39.2	382	16	US-10-735-019-6
9	783.5	39.2	382	16	US-10-734-778-6
10	783.5	39.2	382	16	US-10-735-442-6
11	783.5	39.2	382	17	US-10-848-307-4

12	783.5	39.2	382	17	US-10-886-906-6	Sequence 6, Appli
13	766	38.3	389	16	US-10-808-807-6	Sequence 6, Appli
14	760	38.0	387	17	US-10-810-723-8	Sequence 8, Appli
15	759	38.0	388	16	US-10-804-677-6	Sequence 6, Appli
16	757	37.9	388	16	US-10-808-979-6	Sequence 6, Appli
17	195.5	9.8	420	16	US-10-451-793-59	Sequence 59, Appli
18	195.5	9.8	501	9	US-09-323-998D-55	Sequence 55, Appli
19	195.5	9.8	515	15	US-10-425-114-40728	Sequence 40728, A
20	191.5	9.6	419	16	US-10-451-793-68	Sequence 68, Appli
21	177	8.9	418	16	US-10-451-793-69	Sequence 69, Appli
22	174.5	8.7	397	14	US-10-156-761-8560	Sequence 8560, Ap
23	170.5	8.5	418	16	US-10-451-793-61	Sequence 61, Appli
24	170.5	8.5	498	9	US-09-323-998D-57	Sequence 57, Appli
25	163.5	8.2	502	16	US-10-451-793-63	Sequence 63, Appli
26	163.5	8.2	502	9	US-09-323-998D-56	Sequence 56, Appli
27	161.5	8.1	418	16	US-10-451-793-60	Sequence 60, Appli
28	161.5	8.1	500	9	US-09-323-998D-58	Sequence 58, Appli
29	161	8.1	418	16	US-10-451-793-62	Sequence 62, Appli
30	161	8.1	500	9	US-09-323-998D-59	Sequence 59, Appli
31	159	8.0	418	16	US-10-451-793-66	Sequence 66, Appli
32	157.5	7.9	422	16	US-10-451-793-64	Sequence 64, Appli
33	157.5	7.9	511	9	US-09-323-998D-60	Sequence 60, Appli
34	156.5	7.8	370	16	US-10-425-115-237207	Sequence 237207,
35	150.5	7.5	376	14	US-10-128-713A-20	Sequence 20, Appli
36	150.5	7.5	376	17	US-10-886-906-50	Sequence 50, Appli
37	145	7.3	418	16	US-10-451-793-67	Sequence 67, Appli
38	139	7.0	451	17	US-10-866-089-8	Sequence 8, Appli
39	137	6.9	417	16	US-10-451-793-65	Sequence 65, Appli
40	137	6.9	503	9	US-09-323-998D-61	Sequence 61, Appli
41	136	6.8	493	15	US-10-424-559-272683	Sequence 272683,
42	131.5	6.6	353	15	US-10-425-114-52568	Sequence 52568, A
43	127	6.4	456	9	US-09-323-998D-70	Sequence 20, Appli
44	126.5	6.3	422	16	US-10-451-793-75	Sequence 75, Appli
45	126.5	6.3	526	9	US-09-323-998D-53	Sequence 53, Appli

ALIGNMENTS

RESULT 1
US-09-547-267-7
Sequence 7, Application US/09547267
Patent No. US2002014737A1
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasmontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170

TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-547-267-7

Query Match 100.0%; Score 1999; DB 9; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.1e-193;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHDILLIAGAGISGALLIAVDRRPPDARIYMLDARSGPSDOHTWSCDPTDLSPEWMLARL 60
DB 1 MSHDILLIAGAGISGALLIAVDRRPPDARIYMLDARSGPSDOHTWSCDPTDLSPEWMLARL 60
QY 61 SPIRGEMTDEVAFPDHSRRLTTGYSIEAGALIGLQGVDLRMNTHVATLDDTGATLT 120
DB 61 SPIRGEMTDEVAFPDHSRRLTTGYSIEAGALIGLQGVDLRMNTHVATLDDTGATLT 120
QY 121 DGSRIEACVIDARGAVETPHLTGFKVGEIETDAPHGERPMINDATVPQMDGYRF 180
DB 121 DGSRIEACVIDARGAVETPHLTGFKVGEIETDAPHGERPMINDATVPQMDGYRF 180
QY 181 IYLLPFSPTRLIEBTRYSDDGDLDDGALAQASLDYARRGWTGQEMRREGILPIALAH 240
DB 181 IYLLPFSPTRLIEBTRYSDDGDLDDGALAQASLDYARRGWTGQEMRREGILPIALAH 240
QY 241 DAIGWRDHAQAVPVGAGLFHPVTGYSLPYAAQVADAIARDLTTASARRAVGMAI 300
DB 241 DAIGWRDHAQAVPVGAGLFHPVTGYSLPYAAQVADAIARDLTTASARRAVGMAI 300
QY 301 DRADRDRLRLNMLFRGCPDRRYRLQRFYRLPOLIERFYAGRLTLADRLRIYVGR 360
DB 301 DRADRDRLRLNMLFRGCPDRRYRLQRFYRLPOLIERFYAGRLTLADRLRIYVGR 360
QY 361 PPIPLSQAVRCLPERPLQERA 382
DB 361 PPIPLSQAVRCLPERPLQERA 382

RESULT 2
US-09-920-923-5
Sequence 5, Application US/09920923
Publication No. US20030022273A1
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentative Carotenoid
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US/09/920,923
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 382
TYPE: PRT
ORGANISM: Flavobacterium sp. R1534
US-09-920-923-5

Query Match 100.0%; Score 1999; DB 10; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.1e-193;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSHDILLIAGAGISGALLIAVDRRPPDARIYMLDARSGPSDOHTWSCDPTDLSPEWMLARL 60

QY 61 SPIRGEMTDEVAFPDHSRRLTTGYSIEAGALIGLQGVDLRMNTHVATLDDTGATLT 120
DB 61 SPIRGEMTDEVAFPDHSRRLTTGYSIEAGALIGLQGVDLRMNTHVATLDDTGATLT 120
QY 121 DGSRIEACVIDARGAVETPHLTGFKVGEIETDAPHGERPMINDATVPQMDGYRF 180
DB 121 DGSRIEACVIDARGAVETPHLTGFKVGEIETDAPHGERPMINDATVPQMDGYRF 180
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DB 181 IYLLPFSPTRLIEBTRYSDDGDLDDGALAQASLDYARRGWTGQEMRREGILPIALAH 240
QY 241 DAIGWRDHAQAVPVGAGLFHPVTGYSLPYAAQVADAIARDLTTASARRAVGMAI 300
DB 241 DAIGWRDHAQAVPVGAGLFHPVTGYSLPYAAQVADAIARDLTTASARRAVGMAI 300
QY 301 DRADRDRLRLNMLFRGCPDRRYRLQRFYRLPOLIERFYAGRLTLADRLRIYVGR 360
DB 301 DRADRDRLRLNMLFRGCPDRRYRLQRFYRLPOLIERFYAGRLTLADRLRIYVGR 360
QY 361 PPIPLSQAVRCLPERPLQERA 382
DB 361 PPIPLSQAVRCLPERPLQERA 382

RESULT 3
US-10-695-980-5
Sequence 5, Application US/10695980
Publication No. US20040058410A1
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C98435/125944)
CURRENT FILING DATE: 2003-10-29
PRIOR APPLICATION NUMBER: US/10/695,980
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 382
TYPE: PRT
ORGANISM: Flavobacterium sp. R1534
US-10-695-980-5

Query Match 100.0%; Score 1999; DB 15; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.1e-193;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSHDILLIAGAGISGALLIAVDRRPPDARIYMLDARSGPSDOHTWSCDPTDLSPEWMLARL 60
QY 61 SPIRGEMTDEVAFPDHSRRLTTGYSIEAGALIGLQGVDLRMNTHVATLDDTGATLT 120
DB 61 SPIRGEMTDEVAFPDHSRRLTTGYSIEAGALIGLQGVDLRMNTHVATLDDTGATLT 120
QY 121 DGSRIEACVIDARGAVETPHLTGFKVGEIETDAPHGERPMINDATVPQMDGYRF 180
DB 121 DGSRIEACVIDARGAVETPHLTGFKVGEIETDAPHGERPMINDATVPQMDGYRF 180
QY 181 IYLLPFSPTRLIEBTRYSDDGDLDDGALAQASLDYARRGWTGQEMRREGILPIALAH 240
DB 181 IYLLPFSPTRLIEBTRYSDDGDLDDGALAQASLDYARRGWTGQEMRREGILPIALAH 240
QY 241 DAIGWRDHAQAVPVGAGLFHPVTGYSLPYAAQVADAIARDLTTASARRAVGMAI 300
DB 241 DAIGWRDHAQAVPVGAGLFHPVTGYSLPYAAQVADAIARDLTTASARRAVGMAI 300

QY 301 DRAADRFLRLNMLFRGCPDRRRLQRFYRLQFRLRYFVAGRLTLADRLRVTCR 360
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QY 361 PPIPLSOAVRCLPERPLQERA 382
DB 361 PPIPLSOAVRCLPERPLQERA 382

RESULT 4

US-09-941-947A-30
; Sequence 30, Application US/09941947A
; Publication No. US20030003528A1
; GENERAL INFORMATION:
; APPLICANT: Brzostowicz, Patricia C.
; APPLICANT: Cheng, Qiong
; APPLICANT: Dicosimo, Deana J.
; APPLICANT: Koffas, Mattheos
; APPLICANT: Miller, Edward S. Jr.
; APPLICANT: Odom, J. Martin
; APPLICANT: Picataggio, Steve
; APPLICANT: Rouviere, Pierre B.
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: CI.903 US NA
; CURRENT APPLICATION NUMBER: US/09/941,947A
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,858
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Pantoea stewartii
US-09-941-947A-30

Query Match 39.2%; Score 783.5; DB 10; Length 382;
Best Local Similarity 43.7%; Pred. No. 2.7e-70;
Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6;
QY 3 HLLIAGAGLGGALALAVRDRRPARIVMLDARSQSPDOHTWSCHDITLS--PEWTLAR 59
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QY 60 LSPIRGEWTDQEVAFPDHSRRLTTGYSIEAGALIGLQ--GVDLRNTHVATLDDTG 116
DB 64 --PLVVHMPDYQVAFQRRRHVNSGYCVTSRHFAGILRQOFGHLMHTVSAVHAES 121
QY 117 ATLTCGRLEAACYDARGAVETPHLTGFGQFVGEIETDAPHGVERPMINDATVPQND 176
DB 122 VOLADGRILIHASTVIDRGYTPDSALRVGFAFIQGEWQLSAPHGISPIINDATVDOON 181
QY 177 GYRFIYLLPFSPTRLIEPTRYSDGDLDDGALAQASLDYARRGWTOE--MRBRGILP 235
DB 182 GYRFYTLPLSATLIEPTHTYIDKANLQAEARQIRYARQGPLOTTLREBGALP 241
QY 236 IALADATGFWRDHQAQAVPGIAGLFFPVYGSILPYAAQVADAIARDL--TTASARRA 294
DB 242 IITLGDNRQFWQOQOQAC--SGLRAGLFFPTTGYSLPLAVALADRLSALDVTSSVHOT 299
QY 295 VAGMAIDRADRDRLFLNMLFRGCPDRRRLQRFYRLQFRLRYFVAGRLTLADRL 354
DB 300 IAHFAQOERWQOQGFPMNLNMLFLAGPASERWKRVWQRFYGLBEDLIARFYAGKLTVDRL 359
QY 355 RIVTGRPPIPLSOAVRCL 372
DB 360 RILSGKPPVPVFAALQAI 377

RESULT 5
US-10-218-118-6

; Sequence 6, Application US/10218118
; Publication No. US20030148319A1
; GENERAL INFORMATION:
; APPLICANT: Brzostowicz, Patricia
; APPLICANT: Rouviere, Pierre
; APPLICANT: Picataggio, Stephen
; APPLICANT: Cheng, Qiong
; TITLE OF INVENTION: Genes Encoding Carotenoid Compounds
; FILE REFERENCE: CI.1876 US NA
; CURRENT APPLICATION NUMBER: US/10/218,118
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/312,646
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Pantoea stewartii
US-10-218-118-6

Query Match 39.2%; Score 783.5; DB 14; Length 382;
Best Local Similarity 43.7%; Pred. No. 2.7e-70;
Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6;
QY 3 HLLIAGAGLGGALALAVRDRRPARIVMLDARSQSPDOHTWSCHDITLS--PEWTLAR 59
DB 5 YDLIVGAGLNGALALRLQOQHPDKRILILIEGAPAGNHTWSFHEBDITLNOHRMIA- 63
QY 60 LSPIRGEWTDQEVAFPDHSRRLTTGYSIEAGALIGLQ--GVDLRNTHVATLDDTG 116
DB 64 --PLVVHMPDYQVAFQRRRHVNSGYCVTSRHFAGILRQOFGHLMHTVSAVHAES 121
QY 117 ATLTCGRLEAACYDARGAVETPHLTGFGQFVGEIETDAPHGVERPMINDATVPQND 176
DB 122 VOLADGRILIHASTVIDRGYTPDSALRVGFAFIQGEWQLSAPHGISPIINDATVDOON 181
QY 177 GYRFIYLLPFSPTRLIEPTRYSDGDLDDGALAQASLDYARRGWTOE--MRBRGILP 235
DB 182 GYRFYTLPLSATLIEPTHTYIDKANLQAEARQIRYARQGPLOTTLREBGALP 241
QY 236 IALADATGFWRDHQAQAVPGIAGLFFPVYGSILPYAAQVADAIARDL--TTASARRA 294
DB 242 IITLGDNRQFWQOQOQAC--SGLRAGLFFPTTGYSLPLAVALADRLSALDVTSSVHOT 299
QY 295 VAGMAIDRADRDRLFLNMLFRGCPDRRRLQRFYRLQFRLRYFVAGRLTLADRL 354
DB 300 IAHFAQOERWQOQGFPMNLNMLFLAGPASERWKRVWQRFYGLBEDLIARFYAGKLTVDRL 359
QY 355 RIVTGRPPIPLSOAVRCL 372
DB 360 RILSGKPPVPVFAALQAI 377

RESULT 6
US-10-363-567-30
; Sequence 30, Application US/10363567
; Publication No. US20040077068A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours & Company
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: CI.903 PCT
; CURRENT APPLICATION NUMBER: US/10/363,567
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US 60/229858
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/229907
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 382
; TYPE: PRT

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/ ORGANISM: Pantoea stewartii
US-10-363-567-30

Query Match      39.2%; Score 783.5; DB 15; Length 382;
Best Local Similarity 43.7%; Pred. No. 2.7e-70;
Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6;

QY 3 HDLLIAGAGLGGALIALAVRDRRPARIVMLDARSGPSDQHTWSCHDTDL$---PEWILAR 59
DB 5 YDLIIIVGAGLANGLIALRLQOOHPDMRILLIEAGPEAGNHTWSFHEEDLTLNQHRTIA- 63
QY 60 LSPIRGEMTDOEVAFPDHSRRLTTGYGSIKAGALIGLIQ---GVDLRNTHVATLDDTG 116
DB 64 --PLVVHMPDYQVRFPPQRRHNVSGYCVTSRHPAGILRQOFGHLMHTAVSAVHBS 121
QY 117 ATLTDGSRIEACVADAGAVETPHLTVGFOKVGVEIETDAPHGVERPMIDATVPQMD 176
DB 122 VOLADGRIIHASTVIDGKRYTPDSALRVGFQAFIGQEWQLSAPHGLSSPILMDATVPQON 181
QY 177 GYRFYTLPLSATALLIEDTHYIDKANLQABERARQINIDYARQOWPLQTLIREQGLP 235
DB 182 GYRFYTLPLSATALLIEDTHYIDKANLQABERARQINIDYARQOWPLQTLIREQGLP 241
QY 236 IALAHDAIGFMRDHAQAVPVGLAGLPHPTGYSLPYAAQVADAIARDL-TTASARBA 294
DB 242 IITLGDNRQFWQOQPOAC--SGLRAGLPHPTGYSLPYALADRLSLADVFTSSVHQT 299
QY 295 VRGMAIDRADDRLFRILNRLMFLRGCPDRRYRLRQRYRLPOPLIERFYAGRLTLARL 354
DB 300 IAHFAQQRWQOQGFPRMNLRLFLAGPASHRWVRQRYGLPEDLIARFYAGKLVTDRL 359
QY 355 RIVTGRPPILPSQAVRCL 372
DB 360 RILSGKPPVPVPAALQAI 377

RESULT 7
US-10-466-656-4
/ Sequence 4, Application US/1046656
/ Publication No. US20040078846A1
/ GENERAL INFORMATION:
/ APPLICANT: desouza, Mervyn L.
/ APPLICANT: Schroeder, William A.
/ APPLICANT: Kollmann, Sherry R.
/ APPLICANT: May, Colleen A.
/ TITLE OF INVENTION: Carotenoid Biosynthesis
/ FILE REFERENCE: 12794-004US1
/ CURRENT APPLICATION NUMBER: US/10/466,656
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: US 60/288,984
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: US 60/264,329
/ PRIOR FILING DATE: 2001-01-26
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 382
/ TYPE: PRT
/ ORGANISM: Pantoea stewartii
US-10-466-656-4

Query Match      39.2%; Score 783.5; DB 15; Length 382;
Best Local Similarity 43.7%; Pred. No. 2.7e-70;
Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6;
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QY 117 ATLTDGSRIEACVADAGAVETPHLTVGFOKVGVEIETDAPHGVERPMIDATVPQMD 176
DB 122 VOLADGRIIHASTVIDGKRYTPDSALRVGFQAFIGQEWQLSAPHGLSSPILMDATVPQON 181
QY 177 GYRFYTLPLSATALLIEDTHYIDKANLQABERARQINIDYARQOWPLQTLIREQGLP 235
DB 182 GYRFYTLPLSATALLIEDTHYIDKANLQABERARQINIDYARQOWPLQTLIREQGLP 241
QY 236 IALAHDAIGFMRDHAQAVPVGLAGLPHPTGYSLPYAAQVADAIARDL-TTASARBA 294
DB 242 IITLGDNRQFWQOQPOAC--SGLRAGLPHPTGYSLPYALADRLSLADVFTSSVHQT 299
QY 295 VRGMAIDRADDRLFRILNRLMFLRGCPDRRYRLRQRYRLPOPLIERFYAGRLTLARL 354
DB 300 IAHFAQQRWQOQGFPRMNLRLFLAGPASHRWVRQRYGLPEDLIARFYAGKLVTDRL 359
QY 355 RIVTGRPPILPSQAVRCL 372
DB 360 RILSGKPPVPVPAALQAI 377

RESULT 8
US-10-735-019-6
/ Sequence 6, Application US/10735019
/ Publication No. US20040191863A1
/ GENERAL INFORMATION:
/ APPLICANT: E. I. duPont de Nemours and Company, Inc.
/ APPLICANT: Suh, Wonchul
/ TITLE OF INVENTION: Mutations affecting Plasmid Copy Number
/ FILE REFERENCE: CI2029 US NA
/ CURRENT APPLICATION NUMBER: US/10/735,019
/ CURRENT FILING DATE: 2003-12-12
/ PRIOR APPLICATION NUMBER: US 60/434973
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 6
/ LENGTH: 382
/ TYPE: PRT
/ ORGANISM: Pantoea stewartii
US-10-735-019-6

Query Match      39.2%; Score 783.5; DB 16; Length 382;
Best Local Similarity 43.7%; Pred. No. 2.7e-70;
Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6;

QY 3 HDLLIAGAGLGGALIALAVRDRRPARIVMLDARSGPSDQHTWSCHDTDL$---PEWILAR 59
DB 5 YDLIIIVGAGLANGLIALRLQOOHPDMRILLIEAGPEAGNHTWSFHEEDLTLNQHRTIA- 63
QY 60 LSPIRGEMTDOEVAFPDHSRRLTTGYGSIKAGALIGLIQ---GVDLRNTHVATLDDTG 116
DB 64 --PLVVHMPDYQVRFPPQRRHNVSGYCVTSRHPAGILRQOFGHLMHTAVSAVHBS 121
QY 117 ATLTDGSRIEACVADAGAVETPHLTVGFOKVGVEIETDAPHGVERPMIDATVPQMD 176
DB 122 VOLADGRIIHASTVIDGKRYTPDSALRVGFQAFIGQEWQLSAPHGLSSPILMDATVPQON 181
QY 177 GYRFYTLPLSATALLIEDTHYIDKANLQABERARQINIDYARQOWPLQTLIREQGLP 235
DB 182 GYRFYTLPLSATALLIEDTHYIDKANLQABERARQINIDYARQOWPLQTLIREQGLP 241
QY 236 IALAHDAIGFMRDHAQAVPVGLAGLPHPTGYSLPYAAQVADAIARDL-TTASARBA 294
DB 242 IITLGDNRQFWQOQPOAC--SGLRAGLPHPTGYSLPYALADRLSLADVFTSSVHQT 299
QY 295 VRGMAIDRADDRLFRILNRLMFLRGCPDRRYRLRQRYRLPOPLIERFYAGRLTLARL 354
DB 300 IAHFAQQRWQOQGFPRMNLRLFLAGPASHRWVRQRYGLPEDLIARFYAGKLVTDRL 359
QY 355 RIVTGRPPILPSQAVRCL 372
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[illegible]

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; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Pantoea stewartii
US-10-735-442-6

Query Match      39.2%; Score 783.5; DB 16; Length 382;
Best Local Similarity 43.7%; Pred. No. 2.7e-70;
Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6;

OY      HDLLIAGAGSGLALIALAVNRPRDARIIVMDARSGPSDDHTWCHDTDL$---PENTLAR 59
        :|::|||::|||:::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       5 YDLILVAGLGLANGLIARLQOOHPDKMLILIEAPEKAGGNHTWSFFHEEDLTINQHRMIA- 63
        |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      LSPIRGEMTDOEVAFPDPDSRRLTTGGSGISEAGALIGLLQ---GVDLRMNTHVALTLDDTG 116
        |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       64 --PLVHHMPDYQVRFPQRHNVNSGYCVTSRNPAGILRLQGPFQGHMLHTAIVASVNHSS 121
        |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      117 ATLDGSRIEAACVIADARGAVEPHLTVGFQKFVGEIETDAPGVBERPMIMDATVPOMD 176
        |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       122 VOLADGRIRIHASTVIDRGYPDLSLVGFQAFIGESWQSAPRGLSSPIIMDAITVDON 181
        |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      177 GYRTIYLPSPTILLIEDTFYSQGLDDQALAOALSIDVARRGWGQE-MRRERGILP 235
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       182 GYRVVTYLPISATALLIEDHYIDKAMLOAERARONIRDVARQSWPLQTLREBQALP 241
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      236 IALHDAIIGFRIDAQGAQVPGGLGAGLFHPPTYGSLPYAAOVADAIALARDL-TTASARRA 294
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       242 ITLVGDNRQFQQQPQAC--SGLAAGLFHPTTGSPLPAVALADRSLSDVFTSSVHQ 299
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      295 VRGMAIDRADRDRLRLNLNMFRCPPDRRYLLQRFYRLPQLIERFYAGRLLTLADRL 354
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       300 IAHFAQQRWQOGQGFRRMLNRLFLAGPAESRWVRVMQSFYGPLEDLIAFYAGKLTVTDRL 359
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      355 RIIVGRPIIPLSQVRCL 372
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       360 RILSKPEPVVFALQAI 377
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT.11
US-10-848-307-4
; Sequence 4, Application US/10848307
; Publication No. US20050003474A1
; GENERAL INFORMATION:
; APPLICANT: desouza, Mervyn L.
; APPLICANT: Schroeder, William A.
; APPLICANT: Kohlmann, Sherry R.
; APPLICANT: May, Colleen A.
; TITLE OF INVENTION: Carotencoid Biosynthesis
; FILE REFERENCE: CGLO/0243US02
; CURRENT APPLICATION NUMBER: US/10/848,307
; CURRENT FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 10/466,656
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/288,984
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/264,329
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Pantoea stewartii
US-10-848-307-4

Query Match      39.2%; Score 783.5; DB 17; Length 382;
Best Local Similarity 43.7%; Pred. No. 2.7e-70;
Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6;

```

QY 3 HDLLIAAGSGALLIALAIVDRRDPDARIWLDARSQSPQHTWSCSDTLTS---PEWLA 59
Db 5 YDLTLVAGIANGILIRLLQOOQHPRKRLITLIEGCPAAGNHTWSFHEEDLTIANQHRMLA- 63
QY 60 LSPIRGEWTDQVEAFEDHSRRRLTTGYSIEAGALIGLLQ---GVDLRNTHVATLDDTG 116
Db 64 --PLVNHMPDYQRFPRQRRHNSGYCYTSHFAGILIRQOQCGMLHTVASVHAES 121
QY 117 ATLTDGSRIEACYIIDARGAVETPHLTVFGQKVVGYEITDAPHGYERMLINDATYPPOND 176
Db 122 VOLADGRIIHASTYIDRGYTPDSALRVGFQAFETIGEBWOLSAFHSISDEIMDATVDOON 181
QY 177 GYRFTYLLPESPRTIILEDRTYSDDGLDDGALAAQASLDVAARSGTGE-WRRERGIIP 235
Db 182 GYRVTYLLPESATMLIEDHTYIDKALQAEARQVIRIDYARQGPLOTILIREOGALIP 241
QY 236 IALAHDAIGFWRBHAQAVPVGAGLGFHVVTGYSLPYAAQVADATIAARDL--TTASARPA 294
Db 242 ITLLGDNRQFQWQQPQAC--SGLRAGLFHHTTYSLPPLAVALADRSLADVFTSSVHOT 299
QY 295 VRGMAIDRADRDRLRLINLNMFLFRGCPDDBRRYLLORFRLPOPILIERYYAGRLTLADRL 354
Db 300 IAHFAQORWQOQGGFFRMLNMLFLAGBASRMEVMORFYGLPEDLITARFAGKLTVTDRL 359
QY 355 RIYVGRPPIPLSQAVRCL 372
Db 360 RILSGKRPVPVFALQAI 377

RESULT 12
US-10-886-906-6
; Sequence 6, Application US/10886906
; Publication No. US20050019852A1

```

: APPLICANT: Sun, Monchul
: APPLICANT: Rouviere, Pierre
: APPLICANT: Cheng, Qiong
: APPLICANT: Tao, Luan
: TITLE OF INVENTION: Production of Aromatic Carotenoids in Gram Negative Bacteria
: FILE REFERENCE: C12128 US NA
: CURRENT APPLICATION NUMBER: US/10/886,906
: CURRENT FILING DATE: 2004-07-08
: PRIORITY APPLICATION NUMBER: US 60/486,106
: PRIORITY FILING DATE: 2003-07-10
: NUMBER OF SEQ ID NOS: 57
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 6
: LENGTH: 382
: TYPE: PRT
: ORGANISM: Pantoea stewartii
: US-10-886-906-6

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Query Match 39.2%; Score 783.5; DB 17; Length 382;

Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6.

3 HDLLIAGAGLSGALIALAVRDRRPDARIVMLDARSGPSDQHTWSCHDTLS---PEWILAR 59

5 YDLITVGAGLNGLTALPILOOHPPDMRILLTEAGPEAGGNHTWSEHEDTLINORWIA- 63

60 TSPBPGEWTDQVAFBPNHSPBTTCVCSIFACAIIGIIO--GYDIPWNTHTATI DDTG 116

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[illegible]

122 VQPHADGKI ITHSI VLDGKI I FDSATHVGF YAF IGEENUSAFHGBDSFI IIMDAI VDYQN TOT

177 GYKFIYLLPFSPIKRLIEDTKRYSDDGDLDDGALAAQASLDYAAKRWIGQE-MRERKGLLP 235

182 GYRFVYTLPLSATALLIEDTHYIDKANLQÆERARQÑIRDYARQGWPLQTLFREEQGALP 241

236 IALAHDAIGFWRDHAQGA V P V G L G A G L F H P V T G Y S L P Y A Q V A D A I A R D L - T T A S A R R A 294

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Db      242  ITLTGNRQFMQOQPAC--SGLRRGLFHPTTGISLPLAVALADRSLADVFSSVHQT 299
QY      295  VRCMAIDRADRDREFLINRMLFRCCPPDRRYRLQRFYLPOLIEREFYAGLTTLADR 352
Db      300  IAHFAOORQOQOQFFEMLRNMLFLTAGPESRWRVQRFYGLPEDLIAFYAGKLTVDR 358
QY      355  RIVTGRPPIPLGSAVRCL 372
Db      360  RLISGKPEVVFPAALQAT 377

```

RESULT 13
US-10-808-807-6
; Sequence 6, Application US/10808807
; Publication No. US20040253663A1
GENERAL INFORMATION

```

1 APPLICANT: E.I. du Pont de Nemours and Co., Inc.
2 APPLICANT: Cheng, Qiong
3 APPLICANT: Tao, Inan
4 APPLICANT: Sedkova, Natalia
5 TITLE OF INVENTION: GENES ENCODING CAROTENOID COMPOUNDS
6 FILE REFERENCE: C12365 US NA
7 CURRENT APPLICATION NUMBER: US/10/808,807
8 PRIORITY FILING DATE: 2004-03-24
9 PRIOR APPLICATION NUMBER: US 60/477,874
10 PRIORITY FILING DATE: 2003-06-12
11 PRIOR APPLICATION NUMBER: US 60/527,083
12 PRIORITY FILING DATE: 2003-12-03
13 NUMBER OF SEQ ID NOS: 20
14 SOFTWARE: Patentin version 3.2
15 SEQ ID NO 6
16 LENGTH: 389
17 TYPE: PRT
18 ORGANISM: Pantoea agglomerans strain DC404
19 US-10-808-807-6

```

Query Match	38.3%	Score 766;	DB 16;	Length 389;
Best Local Similarity	44.7%;	Pred. No. 1.6e-68;		
Matches 169;	Conservative 62;	Mismatches 133;	Indels 14;	Gaps 9

4 DLIAGAGLSGALIALAVRDRPDARIVMLDARSGPSDQHTWSCHDTLSPEWLARLSPI 63

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Db      5 DLIIVGAGLANGLIAMRLKORHPTLAVLMLECGDAPGNGNHTWSFHQHDITPAQHAWLAPL 64
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64 PRGEWTDQVAFPDHSRRIITGYGSE---AGALLGLQGVDLRWNTHVATLDDTGATL 119

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044

1790 בערך, וזו הייתה תחילתה של המהפכה המדעית.

$\frac{1}{2}$ $\frac{1}{3}$ $\frac{1}{4}$ $\frac{1}{5}$ $\frac{1}{6}$ $\frac{1}{7}$ $\frac{1}{8}$ $\frac{1}{9}$ $\frac{1}{10}$ $\frac{1}{11}$ $\frac{1}{12}$ $\frac{1}{13}$ $\frac{1}{14}$ $\frac{1}{15}$ $\frac{1}{16}$ $\frac{1}{17}$ $\frac{1}{18}$ $\frac{1}{19}$ $\frac{1}{20}$ $\frac{1}{21}$ $\frac{1}{22}$ $\frac{1}{23}$ $\frac{1}{24}$ $\frac{1}{25}$ $\frac{1}{26}$ $\frac{1}{27}$ $\frac{1}{28}$ $\frac{1}{29}$ $\frac{1}{30}$ $\frac{1}{31}$ $\frac{1}{32}$ $\frac{1}{33}$ $\frac{1}{34}$ $\frac{1}{35}$ $\frac{1}{36}$ $\frac{1}{37}$ $\frac{1}{38}$ $\frac{1}{39}$ $\frac{1}{40}$ $\frac{1}{41}$ $\frac{1}{42}$ $\frac{1}{43}$ $\frac{1}{44}$ $\frac{1}{45}$ $\frac{1}{46}$ $\frac{1}{47}$ $\frac{1}{48}$ $\frac{1}{49}$ $\frac{1}{50}$ $\frac{1}{51}$ $\frac{1}{52}$ $\frac{1}{53}$ $\frac{1}{54}$ $\frac{1}{55}$ $\frac{1}{56}$ $\frac{1}{57}$ $\frac{1}{58}$ $\frac{1}{59}$ $\frac{1}{60}$ $\frac{1}{61}$ $\frac{1}{62}$ $\frac{1}{63}$ $\frac{1}{64}$ $\frac{1}{65}$ $\frac{1}{66}$ $\frac{1}{67}$ $\frac{1}{68}$ $\frac{1}{69}$ $\frac{1}{70}$ $\frac{1}{71}$ $\frac{1}{72}$ $\frac{1}{73}$ $\frac{1}{74}$ $\frac{1}{75}$ $\frac{1}{76}$ $\frac{1}{77}$ $\frac{1}{78}$ $\frac{1}{79}$ $\frac{1}{80}$ $\frac{1}{81}$ $\frac{1}{82}$ $\frac{1}{83}$ $\frac{1}{84}$ $\frac{1}{85}$ $\frac{1}{86}$ $\frac{1}{87}$ $\frac{1}{88}$ $\frac{1}{89}$ $\frac{1}{90}$ $\frac{1}{91}$ $\frac{1}{92}$ $\frac{1}{93}$ $\frac{1}{94}$ $\frac{1}{95}$ $\frac{1}{96}$ $\frac{1}{97}$ $\frac{1}{98}$ $\frac{1}{99}$ $\frac{1}{100}$

1. **Introduction**

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DB 184 FVYTLPLSADILLIEDIHILDGPI LDADSARARIA-DIAKQQWQEARLVKEEGALFII 234

238 LAHDAIGFWRD-HAOGAVPV-GLGAGLFHPVTIGSLPYAAQVADALA-ARDLTIASARRA 294

Db 243 LSGDPAFWHQFHHQ---PVSGLRAGLFHATTGYSPLAVRLADRIANAPGLHQGALYQL 299

295 VRGWAIDRADRDRFLRLNNMLFRCPPDRRYRLQRFYRLPPLIERFYAGRLTLADRL 354

Db 300 IADFAARHWQTFRFRLLNRMFLAGTPDQWRVMQRFYQLDEQLIARFYAGQLRSADRA 355

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|::|::|::|::|

RESULT 14

; Sequence 8, Application US/10810733

Query Match	38.0%	Score 760	DB 17	Length 387
Best Local Similarity	44.0%	Pred. No. 6.6e-68		
Matches 168; Conservative	54;	Mismatches 146;	Indels 14;	Gaps 6;

RESULT 15
US-10-804-677-6

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: Sequence 6, Application US/10804677
: Publication No. US20040224383A1
: GENERAL INFORMATION:
: APPLICANT: E.I. duPont de Nemours and Company, Inc.
: APPLICANT: Cheng, Qiong
: APPLICANT: Tao, Luan
: APPLICANT: Sedkova, Natalia
: TITLE OF INVENTION: GENES ENCODING CAROTENOID COMPOUNDS
: FILE REFERENCE: CL2346 US NA
: CURRENT APPLICATION NUMBER: US/10/804,677
: CURRENT FILING DATE: 2004-03-19
: PRIOR APPLICATION NUMBER: US 60/468,596
: PRIOR FILING DATE: 2003-05-07
: PRIOR APPLICATION NUMBER: US 60/527,083
: PRIOR FILING DATE: 2003-12-03
: NUMBER OF SEQ ID NOS: 20

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Query Match	38.0%	Score 759	DB 16	Length 388
Best Local Similarity	43.2%	Pred. No. 8.4e-68		
Matches 163; Conservative	61	Mismatches 143	Indels 10	Gaps 5

[illegible]

Search completed: June 17, 2005, 19:55:52
Job time : 132.394 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 17, 2005, 19:21:35 ; Search time 37.3429 Seconds
(without alignments)
763.623 Million cell updates/sec

Title: US-10-695-980-5

Perfect score: 1999

Sequence: 1 MSHDLLAGAGLSGALIALA.....IPLSQAVRCLPERPLQGRA 382

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1999	100.0	382	3	US-08-660-645A-7
2	1999	100.0	382	3	US-09-298-718-7
3	1999	100.0	382	3	US-09-546-969-7
4	1999	100.0	382	3	US-08-980-832-5
5	1999	100.0	382	4	US-09-547-267-7
6	1999	100.0	382	4	US-09-920-923B-5
7	1452	72.6	386	2	US-08-663-310-6
8	1452	72.6	386	2	US-09-006-491-6
9	1452	72.6	386	1	US-09-335-919-6
10	810.5	40.5	382	1	US-07-783-705A-3
11	713.5	35.7	374	1	US-08-095-726-14
12	713.5	35.7	374	1	US-08-096-623A-14
13	195.5	9.8	501	4	US-09-323-998B-55
14	170.5	8.5	498	4	US-09-323-998B-57
15	163.5	8.2	502	4	US-09-323-998B-56
16	161.5	8.1	500	4	US-09-323-998B-58
17	161	8.1	500	4	US-09-323-998B-59
18	158	7.9	498	3	US-09-134-607A-19
19	157.5	7.9	511	4	US-09-801-641-2
20	157.5	7.9	511	4	US-09-323-998B-60
21	153	7.7	498	3	US-09-134-607A-17
22	153	7.7	498	3	US-09-134-607A-18
23	137	6.9	503	4	US-09-323-998B-61
24	132	6.6	498	2	US-08-702-598-2
25	127	6.4	456	4	US-08-624-125-20
26	127	6.4	456	4	US-08-937-155-20
27	126.5	6.3	526	4	US-09-323-998B-53

28	123.5	6.2	411	1	US-08-399-561-2	Sequence 2, Appl
29	122	6.1	524	1	US-08-624-125-2	Sequence 2, Appl
30	122	6.1	524	1	US-08-624-125-21	Sequence 21, Appl
31	122	6.1	524	4	US-08-937-155-2	Sequence 2, Appl
32	122	6.1	524	4	US-08-937-155-21	Sequence 21, Appl
33	122	6.1	524	4	US-09-323-998B-2	Sequence 2, Appl
34	122	6.1	524	4	US-09-323-998B-49	Sequence 49, Appl
35	119	6.0	524	4	US-09-323-998B-21	Sequence 21, Appl
36	118.5	5.9	533	4	US-09-323-998B-26	Sequence 26, Appl
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38	113	5.7	529	4	US-09-323-998B-23	Sequence 23, Appl
39	113	5.7	529	4	US-09-323-998B-47	Sequence 47, Appl
40	113	5.7	529	4	US-09-323-998B-50	Sequence 50, Appl
41	112	5.6	378	4	US-09-323-998B-25	Sequence 25, Appl
42	112	5.6	378	4	US-09-323-998B-48	Sequence 48, Appl
43	112	5.6	426	4	US-09-252-991A-27522	Sequence 27522, A
44	111	5.6	374	4	US-09-323-998B-27	Sequence 27, Appl
45	111	5.6	516	3	US-09-201-641-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-660-645A-7

; Sequence 7, Application US/08660645A

; Patent No. 6087152

; GENERAL INFORMATION:

; APPLICANT: Hohmann, Hans-Peter

; APPLICANT: Pasamontes, Luis

; APPLICANT: Tessier, Michel

; APPLICANT: van Loon, Adolphus

; TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hoffmann-La Roche Inc.

; STREET: 340 Kingsland Street

; CITY: Nutley

; STATE: NJ

; COUNTRY: USA

; ZIP: 07110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/660,645A

; FILING DATE: 07-JUN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95108888.9

; FILING DATE: 09-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Pokras, Bruce A.

; REGISTRATION NUMBER: 32,748

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (201) 235-5801

; TELEFAX: (201) 235-2363

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 382 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-660-645A-7

Query Match 100.0%; Score 1999; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.56-211;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSHDLLIAGAGISGALLAVALVDRPPDARIYMLDARSGPSDQHTWSCHDTLSPFWLRL 60
QY 61 SPIRGEMTDOEVAAPPDHSRLITGYSIEAGALIGLQGVDLRNTHVATLDDTGATLT 120
DB 61 SPIRGEMTDOEVAAPPDHSRLITGYSIEAGALIGLQGVDLRNTHVATLDDTGATLT 120
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DB 121 DGSRIEACVIDARGAVETPHLTVGFQKFGVEIETDAPHGVERPMINDATVPQMDGYRF 180
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DB 181 IYLLPFSPFTRLIEBTRYSDDGDLDDGALAQASLDYAARRGWTQEMREREGILPIALAH 240
QY 241 DAIGFWRHQAQAVPVGAGLFPVTVGSLPYAAQVADAIARDLTTASARRAVRGWAI 300
DB 241 DAIGFWRHQAQAVPVGAGLFPVTVGSLPYAAQVADAIARDLTTASARRAVRGWAI 300
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DB 361 PPIPLSQAVRCLPERPILQERA 382

RESULT 2

US-09-298-718-7
; Sequence 7, Application US/09298718
; Patent No. 6124113

GENERAL INFORMATION:

APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolpheus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,718
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-298-718-7
Query Match 100.0%; Score 1999; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.5e-211;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHDLLIAGAGISGALLAVALVDRPPDARIYMLDARSGPSDQHTWSCHDTLSPFWLRL 60
DB 1 MSHDLLIAGAGISGALLAVALVDRPPDARIYMLDARSGPSDQHTWSCHDTLSPFWLRL 60
QY 61 SPIRGEMTDOEVAAPPDHSRLITGYSIEAGALIGLQGVDLRNTHVATLDDTGATLT 120
DB 61 SPIRGEMTDOEVAAPPDHSRLITGYSIEAGALIGLQGVDLRNTHVATLDDTGATLT 120
QY 121 DGSRIEACVIDARGAVETPHLTVGFQKFGVEIETDAPHGVERPMINDATVPQMDGYRF 180
DB 121 DGSRIEACVIDARGAVETPHLTVGFQKFGVEIETDAPHGVERPMINDATVPQMDGYRF 180
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DB 181 IYLLPFSPFTRLIEBTRYSDDGDLDDGALAQASLDYAARRGWTQEMREREGILPIALAH 240
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DB 241 DAIGFWRHQAQAVPVGAGLFPVTVGSLPYAAQVADAIARDLTTASARRAVRGWAI 300
QY 301 DRADDRFLRLNRLFRGCPDPRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIYVGR 360
DB 301 DRADDRFLRLNRLFRGCPDPRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIYVGR 360
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DB 361 PPIPLSQAVRCLPERPILQERA 382

RESULT 3

US-09-546-969-7
; Sequence 7, Application US/09546969
; Patent No. 6207409

GENERAL INFORMATION:

APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolpheus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,969
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-546-969-7

Query Match 100.0%; Score 1999; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.5e-211;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHDLIIAGAGSALIALAVDRDRPDARIWMDARSGSDQHTWSCHDTDISPEWLAAL 60
DB 1 MSHDLIIAGAGSALIALAVDRDRPDARIWMDARSGSDQHTWSCHDTDISPEWLAAL 60
QY 61 SPIRGEWTDQEVAFPDHRRRLTTGYSIEAGALIGLQGVDRMNTHTVATLDDTGATLT 120
DB 61 SPIRGEWTDQEVAFPDHRRRLTTGYSIEAGALIGLQGVDRMNTHTVATLDDTGATLT 120
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DB 121 DGSRIEACVIDARCAVETPHLTGFKQVGEIETDAPHGVERPMIMDATVPQMDGYRF 180
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DB 241 DAIGFWRDHAQAVPVGAGLFHPVTGYSLPYAAQVADAIARDLTTASARRAVAGMAI 300
QY 301 DRADRDRLRLNRLFRGCPDRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIVTGR 360
DB 301 DRADRDRLRLNRLFRGCPDRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIVTGR 360
QY 361 PPIPLSOAVRCLPERPLQERA 382
DB 361 PPIPLSOAVRCLPERPLQERA 382

RESULT 4
US-08-980-832-5
Sequence 5, Application US/08980832B
Patent No. 6231204
GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Teyganikov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentative Carotenoid Production
CURRENT APPLICATION NUMBER: US/08/980,832B
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 382
TYPE: PRT
ORGANISM: Flavobacterium sp. R1534
US-08-980-832-5

Query Match 100.0%; Score 1999; DB 3; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.5e-211;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSHDLIIAGAGSALIALAVDRDRPDARIWMDARSGSDQHTWSCHDTDISPEWLAAL 60
QY 61 SPIRGEWTDQEVAFPDHRRRLTTGYSIEAGALIGLQGVDRMNTHTVATLDDTGATLT 120
DB 61 SPIRGEWTDQEVAFPDHRRRLTTGYSIEAGALIGLQGVDRMNTHTVATLDDTGATLT 120
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DB 121 DGSRIEACVIDARCAVETPHLTGFKQVGEIETDAPHGVERPMIMDATVPQMDGYRF 180
QY 181 IYLLPSPTRILLIEDTRYSDGDLDDGALAQAASLDYAAARGWTGQEMREREGILPTALAH 240
DB 181 IYLLPSPTRILLIEDTRYSDGDLDDGALAQAASLDYAAARGWTGQEMREREGILPTALAH 240
QY 241 DAIGFWRDHAQAVPVGAGLFHPVTGYSLPYAAQVADAIARDLTTASARRAVAGMAI 300
DB 241 DAIGFWRDHAQAVPVGAGLFHPVTGYSLPYAAQVADAIARDLTTASARRAVAGMAI 300
QY 301 DRADRDRLRLNRLFRGCPDRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIVTGR 360
DB 301 DRADRDRLRLNRLFRGCPDRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIVTGR 360
QY 361 PPIPLSOAVRCLPERPLQERA 382
DB 361 PPIPLSOAVRCLPERPLQERA 382

RESULT 5
US-09-547-267-7
Sequence 7, Application US/09547267
Patent No. 6613543
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Teesler, Michel
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-547-267-7

Query Match 100.0%; Score 1999; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.5e-211;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHDLIIAGAGSALIALAVDRDRPDARIWMDARSGSDQHTWSCHDTDISPEWLAAL 60
DB 1 MSHDLIIAGAGSALIALAVDRDRPDARIWMDARSGSDQHTWSCHDTDISPEWLAAL 60

QY 61 SPIRGEWTDQVAPPDHRRLLTGYGSIAGALIGLGGVDLRNNTHTVATLDDTGATLT 120
DB 61 SPIRGEWTDQVAPPDHRRLLTGYGSIAGALIGLGGVDLRNNTHTVATLDDTGATLT 120
QY 121 DGSRIEACVIDARCAVETPHLTGFGQKVGVEIETDAPHGVERPMINDATYPOMDGYRF 180
DB 121 DGSRIEACVIDARCAVETPHLTGFGQKVGVEIETDAPHGVERPMINDATYPOMDGYRF 180
QY 181 IYLLFFSPRILIEPTRYSDDGLDDGALAQASLDYAAARGMTGEMRERGILPLALAH 240
DB 181 IYLLFFSPRILIEPTRYSDDGLDDGALAQASLDYAAARGMTGEMRERGILPLALAH 240
QY 241 DAIGFWRDHAQAVPVGAGLFHPVTGYSLEPYAAQVADAIARDLTTASARAVRGMAI 300
DB 241 DAIGFWRDHAQAVPVGAGLFHPVTGYSLEPYAAQVADAIARDLTTASARAVRGMAI 300
QY 301 DRADDRFLRLNRLMFRCCPPDRRRRLQRFYRLPOPLIERFYAGRLTLADRLRIVTGR 360
DB 301 DRADDRFLRLNRLMFRCCPPDRRRRLQRFYRLPOPLIERFYAGRLTLADRLRIVTGR 360
QY 361 PPIPLSQAVRCLPERPILQERA 382
DB 361 PPIPLSQAVRCLPERPILQERA 382

RESULT 6

US-09-920-923B-5
; Sequence 5, Application US/09920923B
; Patent No. 6677134
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tsygankov, Yuri
; TITLE OF INVENTION: Fermentative Carotenoid Production
; FILE REFERENCE: 15464 US (C39635/125944)
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US/09/920,923B
; PRIOR FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 382
; TYPE: PRF
; ORGANISM: Flavobacterium sp. R1534
US-09-920-923B-5

Query Match 100.0%; Score 1999; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.5e-211;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHDLLIAGAGLIALAVDRRDPARIWMLDARSGPSDQHTWSCDPTDLSPEMLARL 60
DB 1 MSHDLLIAGAGLIALAVDRRDPARIWMLDARSGPSDQHTWSCDPTDLSPEMLARL 60
QY 61 SPIRGEWTDQVAPPDHRRLLTGYGSIAGALIGLGGVDLRNNTHTVATLDDTGATLT 120
DB 61 SPIRGEWTDQVAPPDHRRLLTGYGSIAGALIGLGGVDLRNNTHTVATLDDTGATLT 120
QY 121 DGSRIEACVIDARCAVETPHLTGFGQKVGVEIETDAPHGVERPMINDATYPOMDGYRF 180
DB 121 DGSRIEACVIDARCAVETPHLTGFGQKVGVEIETDAPHGVERPMINDATYPOMDGYRF 180
QY 181 IYLLFFSPRILIEPTRYSDDGLDDGALAQASLDYAAARGMTGEMRERGILPLALAH 240
DB 181 IYLLFFSPRILIEPTRYSDDGLDDGALAQASLDYAAARGMTGEMRERGILPLALAH 240
QY 241 DAIGFWRDHAQAVPVGAGLFHPVTGYSLEPYAAQVADAIARDLTTASARAVRGMAI 300
DB 241 DAIGFWRDHAQAVPVGAGLFHPVTGYSLEPYAAQVADAIARDLTTASARAVRGMAI 300
QY 301 DRADDRFLRLNRLMFRCCPPDRRRRLQRFYRLPOPLIERFYAGRLTLADRLRIVTGR 360
DB 301 DRADDRFLRLNRLMFRCCPPDRRRRLQRFYRLPOPLIERFYAGRLTLADRLRIVTGR 360

DB 301 DRADDRFLRLNRLMFRCCPPDRRRRLQRFYRLPOPLIERFYAGRLTLADRLRIVTGR 360
QY 361 PPIPLSQAVRCLPERPILQERA 382
DB 361 PPIPLSQAVRCLPERPILQERA 382

RESULT 7

US-08-663-310-6
; Sequence 6, Application US/08663310
; Patent No. 5811273
; GENERAL INFORMATION:
; APPLICANT: MISANA, No. 5811273jinhiko
; APPLICANT: KONDO, Keiji
; APPLICANT: KAWIWARA, Susumu
; APPLICANT: YOKOYAMA, Akihito
; TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
; TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,310
; FILING DATE: 23-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/02220
; FILING DATE: 26-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-235917
; FILING DATE: 05-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-348737
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 49441/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 386 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-663-310-6

Query Match 72.6%; Score 1452; DB 2; Length 386;
Best Local Similarity 71.5%; Pred. No. 4.4e-151;
Matches 276; Conservative 40; Mismatches 66; Indels 4; Gaps 2;

QY 1 MSHDLLIAGAGLIALAVDRRDPARIWMLDARSGPSDQHTWSCDPTDLSPEMLARL 60
DB 1 MSHDLLIAGAGLIALAVDRRDPARIWMLDARSGPSDQHTWSCDPTDLSPEMLARL 60
QY 61 SPIRGEWTDQVAPPDHRRLLTGYGSIAGALIGLGGVDLRNNTHTVATLDDTGAT 118
DB 61 SPIRGEWTDQVAPPDHRRLLTGYGSIAGALIGLGGVDLRNNTHTVATLDDTGAT 120

TYPE: amino acid

PRIOR APPLICATION DATA: JP 6-235917
APPLICATION NUMBER:

FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29, 768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-335-919-6

Query Match 72.6%; Score 1452; DB 3; Length 386;
Best Local Similarity 71.5%; Pred. No. 4.4e-151;
Matches 276; Conservative 40; Mismatches 66; Indels 4; Gaps 2;

QY 1 MSHDLLIAGAGISGALIALAVDRRPARIVMLDARSGPSDQHTWSCDPTDISPEMLARL 60
DB 1 VTHDIVLAGAGLANGILIALRAARPDRLVLLDHAAGPSDQHTWSCDPTDISPEMLARL 60
QY 61 SPIRGENTDOVAFPDHSRLTTGYSIEAGALIGLL--QGVDLRMNTHVATLDDTGAT 118
DB 61 KFLRRAMPDOEVRPRHARRLATYGSIDGAALADAVRSGAELRMSDIALDLAOGAT 120
QY 119 LTDGRIEACVTDARGAVETPHLTVGFOKFVGEIETDAPRGVRRPMIMDATTVPQMDGY 178
DB 121 LSCGRIRAGAVLDGRAGQPSRHLTVGQKFVGEIETDPRGVRRPMIMDATTVPQMDGY 180
QY 179 RFIYLLPSPTRILLIEDTRYSDGDLDDGALAQAASLDVYARRGWTQENRRERGILPTAL 238
DB 181 RFIYLLPSPTRILLIEDTRYSDGDLDDGALAQAASLDVYARRGWTQENRRERGILPTAL 240
QY 239 AHDAIGFWRDHAOGAVPVGLAGLPHPTVGYSLPYAAQVADAIARDL--TTASARRAVR 296
DB 241 AHDAIGFWRDHAOGAVPVGLAGLPHPTVGYSLPYAAQVADAIARDL--TTASARRAVR 300
QY 297 GVAIRADDRFLRLNRLFRGCPDRRYRLQRFYRLPOLIRFVYAGRLTLADRLRI 356
DB 301 DYAIRADDRFLRLNRLFRGCPDRRYRLQRFYRLPOLIRFVYAGRLTLADRLRI 360
QY 357 VTGRPIPLSOAVRCLPERPILQERA 382
DB 361 VTGRPIPLSOAVRCLPERPILQERA 386

RESULT 10
US-07-783-705A-3
Sequence 3, Application US/07783705A
Patent No. 5429939
GENERAL INFORMATION:
APPLICANT: Miawa, No. 5429939ihiko
APPLICANT: Kobayashi, Kazuo
APPLICANT: Nakamura, Katsumi
APPLICANT: Yamano, Shigeyuki
TITLE OF INVENTION: DNA SEQUENCES USEFUL FOR THE
TITLE OF INVENTION: SYNTHESIS OF CAROTENOIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ladac & Parry
STREET: 26 West 61 Street
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720Kb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07783, 705A
FILING DATE: 19911023
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1-103078
FILING DATE: 21-APR-1989
APPLICATION NUMBER: JP 2-53225
FILING DATE: 05-MAR-1990
APPLICATION NUMBER: US 07/519, 011
FILING DATE: 19-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schwadron, Janet I.
REGISTRATION NUMBER: 33,778
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-708-1935
TELEFAX: 212-246-5959
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-783-705A-3

Query Match 40.5%; Score 810.5; DB 1; Length 382;
Best Local Similarity 45.6%; Pred. No. 1.9e-80;
Matches 171; Conservative 59; Mismatches 138; Indels 7; Gaps 4;

QY 3 HDLLIAGAGISGALIALAVDRRPARIVMLDARSGPSDQHTWSCDPTDISPEMLARLSP 62
DB 5 YDLIVGAGLANGILIALRLQOQGFPMRLILLDAPRQAGNTHVGHDDLRESQHWIAP 64
QY 63 IRRGEMTQEVAFPDHSRLTTGYSIEAGALIGLLQ--QGVDLRMNTHVATLDDTGAT 119
DB 65 LVHNMPPDYQVRFPRRRKLSNGYFCITSQRFAYELQRFPHLMMDRAVEVNAESVRL 124
QY 120 TDGRIEACVTDARGAVETPHLTVGFOKFVGEIETDAPRGVRRPMIMDATTVPQMDGY 179
DB 125 KKGQVIGRAVYIDGAVANSALSVGFQFTGQEWRLSHPLGLSSPTIMDATTVPQMDGY 184
QY 180 RFIYLLPSPTRILLIEDTRYSDGDLDDGALAQAASLDVYARRGWTQENRRERGILPTAL 238
DB 185 RFIYLLPSPTRILLIEDTRYSDGDLDDGALAQAASLDVYARRGWTQENRRERGILPTAL 244
QY 239 AHDAIGFWRDHAOGAVPVGLAGLPHPTVGYSLPYAAQVADAIARDL--TTASARRAVR 297
DB 245 SGNDAPFQOGRPLAC--SGLRAGLPHPTVGYSLPYAAQVADAIARDL--TTASARRAVR 302
QY 298 WAIDRADDRFLRLNRLFRGCPDRRYRLQRFYRLPOLIRFVYAGRLTLADRLRI 357
DB 303 FARERMOOQGFPRMLNRLFLAGPADSRWQRFGYLEDLIAFVAGKLTLLDRRLIL 362
QY 358 VTGRPIPLSOAVRCL 372
DB 363 VTGRPIPLSOAVRCL 377

RESULT 11
US-08-095-726-14
Sequence 14, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Auslich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharfi, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huei-Che B

TITLE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-095-726-14

Query Match 35.7%; Score 713.5; DB 1; Length 374;
Best Local Similarity 41.5%; Pred. No. 9.1e-70;
Matches 158; Conservative 55; Mismatches 139; Indels 29; Gaps 6;
QY 4 DILLIAGAGLIALAVDRRDPARIWMLDARSGPSDOHTWSCDPTLSPKMLARLSPI 63
DB 3 DILLVGGGLANGLIARLRRORYPQLNLLIEAGEQPGGNHTWSFHEDDITPGQHWLADL 62
QY 64 RRGWTDQVAPDPDSRLITGSGIEAGLIGLQ--GVDLRWTHVATLDDTGATLT 120
DB 63 VAHAWGVEVQPPDLRRRLARGYSITSERFAELHQAALGENIWNCSVSEVLPSVRLA 122
QY 121 DGSRIEACVINDARCAVETPHLTVGQKFGVGEIETDAPHGVERPMINDATVPQMDGYRF 180
DB 123 NBEALLAGAVIDGRGTASAMQGYQLFLGOQWRLTQPHGLTVPLMDATVAQOQGYRF 182
QY 181 IYLLPSPFRLIIESTRYSDDGDLDDGALAQAASLDYAARRGW-TQGEWRERGIPLIALA 239
DB 183 VYTLPLASADTLIEDTRYANVPOQDNDALRQVTVTDVAHSGMQLAQLREBETGCLPIT-- 240
QY 240 HNAIGWRHAGCAVNV-----GLGAGLHPVTGTSLYAAOVADAIA-----ARDLT 287
DB 241 -----WRTSRLICGWRRAASGMAGLPHPTTGSLSLAVALADADSPRLGSVPLY 294
QY 288 TASARAIVAGMAIDRADRFLLRLNRMFLRGCPRRYRLQRFRLPOPLIERFYAGR 347
DB 295 QLTQCEAEHNR-----RGCFRLINRMFLLAGREENRWRVWQRFGLPEPTVERFYAGR 349
QY 348 LTLADRLRIVTGRPPILPSQA 368
DB 350 LSLFDKARILITGKFPVPLAKS 370

RESULT 12
US-08-096-623A-14
Sequence 14, Application US/08096623A
Patent No. 5684238
GENERAL INFORMATION:

APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,613
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REFERENCE/DOCKET NUMBER: 29,381
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 655-1500
TELEFAX: (312) 655-1501
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-096-623A-14

Query Match 35.7%; Score 713.5; DB 1; Length 374;
Best Local Similarity 41.5%; Pred. No. 9.1e-70;
Matches 158; Conservative 55; Mismatches 139; Indels 29; Gaps 6;
QY 4 DILLIAGAGLIALAVDRRDPARIWMLDARSGPSDOHTWSCDPTLSPKMLARLSPI 63
DB 3 DILLVGGGLANGLIARLRRORYPQLNLLIEAGEQPGGNHTWSFHEDDITPGQHWLADL 62
QY 64 RRGWTDQVAPDPDSRLITGSGIEAGLIGLQ--GVDLRWTHVATLDDTGATLT 120
DB 63 VAHAWGVEVQPPDLRRRLARGYSITSERFAELHQAALGENIWNCSVSEVLPSVRLA 122
QY 121 DGSRIEACVINDARCAVETPHLTVGQKFGVGEIETDAPHGVERPMINDATVPQMDGYRF 180
DB 123 NBEALLAGAVIDGRGTASAMQGYQLFLGOQWRLTQPHGLTVPLMDATVAQOQGYRF 182
QY 181 IYLLPSPFRLIIESTRYSDDGDLDDGALAQAASLDYAARRGW-TQGEWRERGIPLIALA 239

Db 183 VTTLLSADTLLIEBTRYANVPQORDNMLRQTVTYTVAHSGKQMLAQLEEEETGCLPIT-- 240
Qy 240 HDAIFWGDHAGAVP-----GLGAGLFEHVTGSLPYAAQVNDATA-----ABDIT 287
Db 241 -----WRTSYLSCGMRRRAASGMAGLFHPTTGLSPLAVALADLSDSRLSVPILY 294
Qy 288 TASARAVAGWAIIDRADRDRLRLNRLFRGCPDPRRYRLQRFYRLPQPLIERFYAGR 347
Db 295 QLTQFPAERHMR-----RQCFRLNRLMLFLAGREENRMRVMQRFYGLPEPTVERFYAGR 349
Qy 348 LTLADRLRLVTGRPPILPSQA 368
Db 350 LSLFDKARILTGKPPVPLAKS 370

RESULT 13
US-09-323-998E-55
; Sequence 55, Application US/09323998E
; Patent No. 6642021
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM JR., FRANCIS X.
; APPLICANT: SUN, ZAIREN
; TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
; FILE REFERENCE: 108172-09019
; CURRENT APPLICATION NUMBER: US/09/323,998E
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 09/088,724
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 09/088,725
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 55
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-323-998E-55

Query Match 9.8%; Score 195.5; DB 4; Length 501;
Best Local Similarity 23.4%; Pred. No. 1.6e-12;
Matches 111; Conservative 66; Mismatches 144; Indels 153; Gaps 27;

Qy 4 DLLIAGAGLIALAIVDRRPPARIYVLDARSGPSDQHTWSCDITLSPFWLARLSPIT 63
Db 84 DLAIYGGGAGLAIVAOQVSE--AGLSVCSID-----PSPKLIW-----PN 121
Qy 64 RRGWTDQ-----EVAFPDH--SRRLTTGYSIEAGALIG-----LIQ 99
Db 122 NVGVWVDFEAMDLLDCLDTTWSGANVYVDGKVDLSRPGRVNRKQKSKMOKCITN 181
Qy 100 GVDLRKN--THYATLDDTGATL--TDGSRIEAACVVDANG-----AVETPHLTVGFQKF 149
Db 182 GKRFHQAKVTNVVH--EENASTVVCSDGVXIQASVLDATGFSRCLVQYDKPY--NPGYQVA 239
Qy 150 VGVETIETA--PHGVERPMIDATVPQMDGY-----RFIYLLPSPTRILIEDTR 197
Db 240 YGIVAEVDGHPDVMQFMWRDKHLDYPELKERNSKIPFLYAMPSSKRIFLEET-- 298
Qy 198 YSDGDDLDGALAQASL-----DYAARRGWVGQEMR-----ERGILPILAHDAIGFW 246
Db 299 -----SLVARPGLRMEDIQERMAARLKHGINVAKIIEEDRCVIMG----- 340
Qy 247 RDHAGAVP-----VGLG--AGLFHPVTGY-----SLPYAAQVADAIARDLTTASARRA 294
Db 341 -----GRLPVLPRQRVVGGTAGMVPSTGYWVARLAAPIVANA1--TRYIGSSSS--NS 393
Qy 295 VNG-----NAIDRADRFLRLNRLFRGCPDPRRYRLQRFYRLPQPLIERFY 343
Db 394 LMGDDLSAEVWMDLWIERRQREFFCFGMDILK--LDIDATRRFPDAFDLQPHYMGF 452
Qy 344 YAGRLTLAD-----RLRIYVGRPPILPSQAVRCLPERPLQER 381

Db 453 LSSRLFELLVFGLSLFSHASNTSRLEIMT--KGVPLAKMI-----NNLQVDR 500

RESULT 14
US-09-323-998E-57
; Sequence 57, Application US/09323998E
; Patent No. 6642021
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM JR., FRANCIS X.
; APPLICANT: SUN, ZAIREN
; TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
; FILE REFERENCE: 108172-09019
; CURRENT APPLICATION NUMBER: US/09/323,998E
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 09/088,724
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 09/088,725
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 57
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Capsicum annum
US-09-323-998E-57

Query Match 8.5%; Score 170.5; DB 4; Length 498;
Best Local Similarity 21.4%; Pred. No. 9e-10;
Matches 101; Conservative 67; Mismatches 154; Indels 149; Gaps 26;

Qy 4 DLLIAGAGLIALA-----LAVDRRPPARIYVLDARSGPSDQHTW-----S 46
Db 83 DLAVGGGAGLAIVAOQVSEAGLSVCSIDPRKLIW-----PNNYGVWVDFEAMDLLD 136
Qy 47 CHDITLSPFWLARLSPIRGWTQEVAFPDHRR--LTTGYGSIIEAGALIG-----LIQ 99
Db 137 CLD-----ATWSGAAYVIDKTYTDKDLNRPYGRVNRKQKSKMOKCITN 180
Qy 100 GVDLRKNTHVATLDDTGATL--TDGSRIEAACVVDANG-----AVETPHLTVGFQKFV 150
Db 181 GKRFHQAKVIVKHESKSMILCNDGITIQATVLDATGFSRSLVQYDKPY--NPGYQVA 239
Qy 151 GV--FIETDPAHGVPRMID-----ATVPQMDGYRFIYLLPSPTRIL 192
Db 240 GILAEVE--EHPDVKVQFMQWRDROSHLKNVIELKERNRIP-----TLVAMPSSNRIF 293
Qy 193 IEDTRY--SDGDDLDGALAQASLDYARRGWVGQEMR-----ERGILPILAHDAIGFW 246
Db 294 LEETSLVARPGLGMD--IQERM--VARLSHLGIKVKSIEEDRCVIMG----- 339
Qy 247 RDHAGAVP-----VGLG--AGLFHPVTGSLPYAAQVADAIARDLTTASARRANG- 297
Db 340 -----GRLPVLPRQRVVGGTAGMVPSTGYWVARLAAPIVANAIIQYLSSESSHSGD 394
Qy 298 -----NAID--RAARDRFLRLNRLFRGCPDPRRYRLQRFYRLPQPLIERFYAG 346
Db 395 ELISAAMVMDLWIERRQREFFCFGMDILKLDLPATRFF--FDAFPLERRYMHGFLSS 452
Qy 347 RLTLAD-----RLRIYVGRPPILPSQAVRCLPERPLQER 381
Db 453 RLFLPELLVFGLSLFSHASNTSRLEIMT--KGTLLPVHMI-----NNLQDK 497

RESULT 15
US-09-323-998E-56
; Sequence 56, Application US/09323998E
; Patent No. 6642021
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM JR., FRANCIS X.
; APPLICANT: SUN, ZAIREN
; TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND

FILE REFERENCE: 108172-09019
CURRENT APPLICATION NUMBER: US/09/323,998E
CURRENT FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 09/088,724
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
LENGTH: 502
TYPE: PRT
ORGANISM: Adonis palaeestina
US-09-323-998E-56

Query Match 8.2%; Score 163.5; DB 4; Length 502;
Best Local Similarity 21.1%; Pred. No. 5.4e-09;
Matches 92; Conservative 61; Mismatches 141; Indels 141; Gaps 22;

QY 4 DLLIAGAGSGLIA-----LAVDRRPDARIWLDARSGPSDQHT-----S 46
DB 87 DLAVVGGGAGLAIQQVSEAGLVCSIDPSPLIW-----PNNGVWVDFEAMDLLD 140
QY 47 CHDTLSPFWLRLSPIRGEWTDQEVAPPDSRR-LTTGYSIEAGALIG-LIQ----- 99
DB 141 CLDT-----TWGAVVYDDNSKTLDRPYGRVNRKQLSKMLQKCTN 184
QY 100 GVDLRMNTVATLDTGATL---TDGSRLEACVIDARG-----AVETPHLTVGFQKFV 150
DB 185 GVKFQAKIVKIYHESKSLICNDGITINATVLDATGFSRCLVQDKPY-NPGYQVAY 243
QY 151 GVEIETDA-PHGEVPMIND-----ATVPQMDGRTFYLLPSPFRI LI 193
DB 244 GIMAEVEBHPFDLQKLFMDWRDShLNEKLEKDKNRKIP-----TFLYAMPFSSSTKIFL 298
QY 194 EDTRYSDGDLDDGALAQASLDY-----AARGWGTQEMR---ERGITLPIALAHDA 242
DB 299 EET-----SLVARGLRPEDIQERMVARLKHGLIKVKSIEEDRCVIFMG----- 343
QY 243 IGFMRDHAQAVP-----VGLG--AGLFHPVTGYSLPYAAQVADADAIAARDLTTASARRA 294
DB 344 -----GRLPVLPRQVVGIGTAGVHPSTGYVAVARTLAAPVAVAKSIVQYLGSDRS 394
QY 295 VAG-----WAIIDRADRDF---LRLNRMLFRGCCPPDRRYRLQRFYRLPQPL 339
DB 395 LSGNELSAEVMKDLMPIERRQREFFCFGMIDILKLDLG-----TRRFDAFFDLBPHY 449
QY 340 IERFYAGRLTLADRL 354
DB 450 WIGFLSSRLFLPELL 464

Search completed: June 17, 2005, 19:39:10
Job time : 39.3429 secs

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OM protein - protein search, using sw model

Run on: June 17, 2005, 18:53:39 ; Search time 140.801 Seconds
(without alignments)
1049.298 Million cell updates/sec

Title: US-10-695-980-5

Perfect score: 1999
Sequence: 1 MSHDLLIAGAGLGGALIALA.....IPLSQAVRCLPFRPLQGERA 382

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1999	100.0	382	2	AAW06517
2	1999	100.0	382	2	AAW06517
3	1456	72.8	386	2	AAW79062
4	1456	72.8	386	2	AAW79062
5	1405	70.3	386	2	AAW9096
6	1405	70.3	386	2	AAW9096
7	810.5	40.5	380	8	ADP74123
8	810.5	40.5	382	2	AAW7445
9	810.5	40.5	382	2	AAW82258
10	810.5	40.5	382	2	AAW87891
11	810.5	40.5	382	2	AAW9100
12	783.5	39.2	382	5	AAE22313
13	783.5	39.2	382	6	AAO16019
14	783.5	39.2	382	6	ABP96687
15	783.5	39.2	382	8	ADQ14629
16	783.5	39.2	382	8	ADQ17204
17	783.5	39.2	382	8	ADQ48639
18	783.5	39.2	382	8	ADQ48639
19	713.5	35.7	374	2	AAW01125
20	713.5	35.7	374	2	AAW24474
21	712.5	35.6	374	2	AAW13987
22	671	27.6	392	6	ABW70122
23	551.5	9.8	434	2	AAW95698
24	195.5	9.8	501	3	AAW54311
25	195.5	9.8	501	3	AAW54311

26	195.5	9.8	501	5	ABW92263	Abp92263 Herbicide
27	194.5	9.7	500	8	ADO05148	Ado05148 A. thalia
28	194.5	9.7	501	8	ADO05224	Ado05224 A. thalia
29	178.5	8.9	411	8	ADH39777	Adh39777 Streptomycin
30	175	8.8	328	3	AAW53413	AAW53413 Arabidopsis
31	175	8.8	369	3	AAW53412	AAW53412 Arabidopsis
32	174.5	8.7	524	8	ADO05152	Ado05152 Citrus X
33	172.5	8.6	524	8	ADO05211	Ado05211 Citrus X
34	170.5	8.5	498	2	AAW06454	AAW06454 Capsicum
35	170.5	8.5	498	3	AAW54313	AAW54313 Amino acid
36	163.5	8.2	502	3	AAW54312	AAW54312 Amino acid
37	161.5	8.1	500	3	AAW54314	AAW54314 Amino acid
38	161.5	8.1	500	8	ADO61088	Ado61088 Tomato be
39	161.5	8.1	500	8	ADP74116	Adp74116 Tomato be
40	161.5	8.1	500	8	ADQ38257	Adq38257 Tomato be
41	161.5	8.1	500	8	ADQ94526	Adq94526 Tomato be
42	158	7.9	498	3	AAW70397	AAW70397 Protein e
43	157.5	7.9	511	3	AAW90226	AAW90226 Marigold
44	157.5	7.9	511	3	AAW54316	AAW54316 Amino acid
45	157	7.9	500	3	AAW54315	AAW54315 Amino acid

ALIGNMENTS

RESULT 1

AAW06517 standard; protein; 382 AA.

XX	AAW06517;					
XX	17-OCT-2003	(revised)				
DT	08-MAR-1997	(first entry)				
XX	Flavobacterium lycopen cyclase.					
XX	Carotenoid; lycopen; beta-carotene; echinenone; canthaxanthin;					
XX	zeaxanthin; adonixanthin; astaxanthin; crt; lycopen synthase.					
OS	Flavobacterium sp. ATCC 21588; WT (ATCC 21588).					
XX	EP747483-A2.					
XX	11-DEC-1996.					
XX	29-MAY-1996;	96EP-00108556.				
XX	09-JUN-1995;	95EP-00108888.				
XX	(HOPF) HOFFMANN LA ROCHE & CO AG F.					
XX	Hohmann H, Pasamontes L, Tessier M, Van Loon A;					
XX	WPI; 1997-023160/03.					
XX	N-PSDB; AAT45143.					
XX	Flavobacterium gene sequences encoding carotenoid biosynthesis enzymes -					
XX	for the production of carotenoid(s), useful in foods and animal feeds.					
XX	Example 2; Fig 7; 80pp; English.					
XX	Lycopene synthase (AAW06517) is the product of the crt gene identified					
XX	in a carotenoid gene cluster (see also AAT45143) of Flavobacterium sp.					
XX	R1534. This 42368 Da protein introduces the beta-ionone rings at both					
XX	sides of lycopene to obtain beta-carotene. Enzymes of the Flavobacterium					
XX	carotenoid biosynthetic pathway (see also AAW06515-18 and AAW00871) can					
XX	be expressed, optionally with Alcaligenes beta-carotene beta-4-oxigenase,					
XX	in host cells for the prodn. of lycopene, astaxanthin, beta-carotene,					
XX	echinenone, zeaxanthin, canthaxanthin and adonixanthin. (Updated on 17-					
XX	OCT-2003 to standardise OS field)					
XX	Sequence 382 AA;					
XX	SO					

Query Match 100.0%; Score 1999; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 9.6e-201;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHDLIAGAGISGALIALAVRRDRPDARIYMLDARSGPSDOHTWSCHDTLSPEMLARL 60
DB 1 MSHDLIAGAGISGALIALAVRRDRPDARIYMLDARSGPSDOHTWSCHDTLSPEMLARL 60

QY 61 SPIRGEMTDOEVAFPDHSRLTTGYSIEAGALIGLQGVLDLNNTHVATLDDTGATLT 120
DB 61 SPIRGEMTDOEVAFPDHSRLTTGYSIEAGALIGLQGVLDLNNTHVATLDDTGATLT 120

QY 121 DGSRIEACVIDARCAVETPHLTGFGKFGVEIETDAPHGVERPMINDATVPQMDGYRF 180
DB 121 DGSRIEACVIDARCAVETPHLTGFGKFGVEIETDAPHGVERPMINDATVPQMDGYRF 180

QY 181 IYLLPSPSTRLLIEDTRYSDGDLDDGALAQASLDYAARRGWTGQEMRREGILPILALH 240
DB 181 IYLLPSPSTRLLIEDTRYSDGDLDDGALAQASLDYAARRGWTGQEMRREGILPILALH 240

QY 241 DAIGFWRDHAQAVPVGLGAGLFHPVTGYSLPYAQVADAIARDLTTASARRAVRGMAI 300
DB 241 DAIGFWRDHAQAVPVGLGAGLFHPVTGYSLPYAQVADAIARDLTTASARRAVRGMAI 300

QY 301 DRADRDRLRLNRMIFRGCPDPRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIYVGR 360
DB 301 DRADRDRLRLNRMIFRGCPDPRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIYVGR 360

QY 361 PPILSQAVRCLPERPILQERA 382
DB 361 PPILSQAVRCLPERPILQERA 382

RESULT 2
AAW69533 standard; protein; 382 AA.
AAW69533;
10-AUG-1999 (first entry)
Flavobacterium sp. R1534 crtY gene product lycopene cyclase.
Carotenoid; pigment; canthaxanthin; R1534; crtB; prephytoene synthase;
crtI; phytoene desaturase; crtY; lycopene cyclase; GGPP synthase; crtB;
crtW2396; beta-carotene beta-oxygenase; food product; fermentation.
Flavobacterium sp.
JP10155497-A.
16-JUN-1998.
02-DEC-1997; 97JP-00348653.
02-DEC-1996; 96EP-00810839.
(HOFF) HOFFMANN LA ROCHE & CO AG F.
WPI, 1998-391048/34.
N-PSDB; AAV40146.
Preparation of carotenoid - comprises fermentation with transformed cell.
Claim 1, Fig 25; 80pp; Japanese.
The invention describes the preparation of carotenoid pigments e.g.
canthaxanthin using a cell transformed by a vector having DNA sequences
(a) to (e) or substantially homologous sequences. (a) a DNA sequence
(crtB) coding GGPP synthase of Flavobacterium sp. R1534; (b) a DNA
sequence (crtB) coding prephytoene synthase of Flavobacterium sp. R1534;
(c) a DNA sequence (crtI) coding phytoene desaturase of Flavobacterium
sp. R1534; (d) a DNA sequence (crtY) coding lycopene cyclase of

CC Flavobacterium sp. R1534, and (e) a DNA sequence (crtW2396) coding beta-
carotene beta-oxygenase of a microbe E-396 (FERM BP-4283). The carotenoid
CC or a carotenoid mixture can also be used in preparation of food products.
CC The method is an improved method of fermentation for carotenoid
CC production
SQ Sequence 382 AA;

Query Match 100.0%; Score 1999; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 9.6e-201;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSHDLIAGAGISGALIALAVRRDRPDARIYMLDARSGPSDOHTWSCHDTLSPEMLARL 60
DB 1 MSHDLIAGAGISGALIALAVRRDRPDARIYMLDARSGPSDOHTWSCHDTLSPEMLARL 60

QY 61 SPIRGEMTDOEVAFPDHSRLTTGYSIEAGALIGLQGVLDLNNTHVATLDDTGATLT 120
DB 61 SPIRGEMTDOEVAFPDHSRLTTGYSIEAGALIGLQGVLDLNNTHVATLDDTGATLT 120

QY 121 DGSRIEACVIDARCAVETPHLTGFGKFGVEIETDAPHGVERPMINDATVPQMDGYRF 180
DB 121 DGSRIEACVIDARCAVETPHLTGFGKFGVEIETDAPHGVERPMINDATVPQMDGYRF 180

QY 181 IYLLPSPSTRLLIEDTRYSDGDLDDGALAQASLDYAARRGWTGQEMRREGILPILALH 240
DB 181 IYLLPSPSTRLLIEDTRYSDGDLDDGALAQASLDYAARRGWTGQEMRREGILPILALH 240

QY 241 DAIGFWRDHAQAVPVGLGAGLFHPVTGYSLPYAQVADAIARDLTTASARRAVRGMAI 300
DB 241 DAIGFWRDHAQAVPVGLGAGLFHPVTGYSLPYAQVADAIARDLTTASARRAVRGMAI 300

QY 301 DRADRDRLRLNRMIFRGCPDPRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIYVGR 360
DB 301 DRADRDRLRLNRMIFRGCPDPRRYRLQRFYRLPQPLIERFYAGRLTLADRLRIYVGR 360

QY 361 PPILSQAVRCLPERPILQERA 382
DB 361 PPILSQAVRCLPERPILQERA 382

RESULT 3
AAR79062 standard; peptide; 386 AA.
AAR79062;
27-AUG-2003 (revised)
28-FEB-1996 (first entry)
3 hydroxy-beta-ionone ring methylene to keto group converting peptide.
Xanthophyll; astaxanthine; methylene; keto group; conversion;
3-hydroxy-beta-ionone ring.
Agrobacterium aurantiacum.
WO9518220-A1.
06-JUL-1995.
26-DEC-1994; 94WO-JP002220.
27-DEC-1993; 93JP-00348737.
05-SEP-1994; 94JP-00235917.
(KIRI) KIRIN BEER KK.
PA (MARI-) MARINE BIOTECHNOLOGY INST CO LTD.
Misawa N, Kondo K, Kajiwara S, Yokoyama A;
WPI, 1995-246386/32.
N-PSDB; AAQ99489.

XX DNA's encoding xanthophyll(s) - esp. astaxanthin and other
 PT xanthophyll(s) using e.g. E. coli.
 XX
 PS Disclosure, Page 21; 131pp; Japanese.
 XX
 CC AAR79058-R790629 are xanthophyll polypeptides. These polypeptides are
 CC capable of converting the 4-methylene group of a 3-hydroxy-beta- ionone
 CC ring to a 4-keto group in doing so these peptides also add a hydroxyl
 CC group to the 3-position carbon-atom of the 4-keto-beta- ionone ring. The
 CC DNA sequences may be used in the production of astaxanthin and other
 CC keto gp. contg. xanthophylls, the sequences may also be used to transform
 CC certain yeasts and other microorganisms. (Updated on 27-AUG-2003 to
 CC correct OS field.)
 CC
 XX Sequence 386 AA;
 SQ
 Query Match 72.8%; Score 1456; DB 2; Length 386;
 Best Local Similarity 71.8%; Pred. No. 1.1e-143;
 Matches 277; Conservative 39; Mismatches 66; Indels 4; Gaps 2;
 QY 1 MSHDLLIAGAGLSGALIALAVRRPPDARIWMDARSGSDQHTWCHDITLSPWLAAL 60
 DB 1 MTHDVLIAAGAGLANGLIALALRAAPDLRLVLLDHAAGSDGHTWCHDITLSPWLAAL 60
 QY 61 SPIRGEWTDQEVAPPDHSRLTTGYGSTEAGALIGLL--QGVDLRMTHTVATLDDTGAT 118
 DB 61 KPIRRANMPDQEVPRFRRARRLATGYGSLDGAALDAVVRSGAEIRWSDILALDAQAT 120
 QY 119 LFDGSRIEACVTDARGAVERPHLTGFOKFVGEIETDAPHGVERPMIMDATVPMQDGY 178
 DB 121 LSCGTRIEAGAVLDGGAQPSRLTVGFOKFVGEIETDRPHGVERPMIMDATVPMQDGY 180
 QY 179 RFTYLLPFSPTRLIEDTRYSDGDLDDGALAQAASLDYARRGWTQEMRRERGLPIAL 238
 DB 181 RFTYLLPFSPTRLIEDTRYSDGDLDDGALAQAASLDYARRGWTQEMRRERGLPIAL 240
 QY 239 AHDAIGFMDHQAQAVPGAGLPHPTGYSLPYAAQVADATA--ARDLTASARRAVR 296
 DB 241 AHDAIGFMDHQAQAVPGAGLPHPTGYSLPYAAQVADAVAGISGPGTDALRGALR 300
 QY 297 GNAIDRADRDRLRLNRLFRGCPDRRYRLQRFYRLPOPLIERFYAGRLTLADRLRI 356
 DB 301 DYALDARDRFLRLNRLFRGCAPDRRYTLQRFYRPHGLIERFYAGRLSVADQLRI 360
 QY 357 VTGRPPILSQAVRCLPERPLQERA 382
 DB 361 VTGKPPILGTALRCLPERPLKENA 386
 RESULT 4
 AAW87884
 ID AAW87884 standard; protein; 386 AA.
 XX
 AC AAW87884;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 DE Protein encoded by the carotenoid biosynthesis gene crtY.
 XX
 KW Carotenoid biosynthesis; astaxanthin diglucoside; crtE gene; crtB gene;
 KW crtI gene; adonixanthin-3'-glucoside; astaxanthin monoglucoside;
 KW carotenoid glycoside; crtY gene; crtZ gene; crtX gene; crtW gene;
 KW food additive.
 XX
 OS Agrobacterium aurantiacum.
 XX
 PN JP10327865-A.
 XX
 PD 15-DEC-1998.
 XX
 PF 29-MAY-1997; 97JP-00140460.
 XX

PR 29-MAY-1997; 97JP-00140460.
 XX
 PA (KIRI) KIRIN BREWERY KK.
 PA (KATY-) KAIYO BIOTECHNOLOGY KENKUTSHO KK.
 XX
 DR WPI; 1999-099030/09.
 DR N-PSDB; AAW87884.
 XX
 PT New carotenoid glucoside(s) - used as food additives.
 PS Disclosure, Page 12-13; 26pp; Japanese.
 XX
 CC The present sequence represents a protein involved in carotenoid
 CC biosynthesis. The specification describes astaxanthin diglucosides and
 CC adonixanthin-3'-glucosides. The specification also describes a method for
 CC the preparation of a carotenoid glycoside, in which all, or part of,
 CC carotenoid biosynthesis genes crtE, crtB, crtI, crtY, crtZ, crtX or crtW
 CC are introduced to a microbe or plant and expressed. The transformed
 CC organism is cultured and astaxanthin diglucosides, adonixanthin-3'-
 CC glucosides, and/or astaxanthin monoglucosides are collected. The
 CC carotenoid glucosides are used as food additives
 CC
 XX Sequence 386 AA;
 SQ
 Query Match 72.8%; Score 1456; DB 2; Length 386;
 Best Local Similarity 71.8%; Pred. No. 1.1e-143;
 Matches 277; Conservative 39; Mismatches 66; Indels 4; Gaps 2;
 QY 1 MSHDLLIAGAGLSGALIALAVRRPPDARIWMDARSGSDQHTWCHDITLSPWLAAL 60
 DB 1 MTHDVLIAAGAGLANGLIALALRAAPDLRLVLLDHAAGSDGHTWCHDITLSPWLAAL 60
 QY 61 SPIRGEWTDQEVAPPDHSRLTTGYGSTEAGALIGLL--QGVDLRMTHTVATLDDTGAT 118
 DB 61 KPIRRANMPDQEVPRFRRARRLATGYGSLDGAALDAVVRSGAEIRWSDILALDAQAT 120
 QY 119 LFDGSRIEACVTDARGAVERPHLTGFOKFVGEIETDAPHGVERPMIMDATVPMQDGY 178
 DB 121 LSCGTRIEAGAVLDGGAQPSRLTVGFOKFVGEIETDRPHGVERPMIMDATVPMQDGY 180
 QY 179 RFTYLLPFSPTRLIEDTRYSDGDLDDGALAQAASLDYARRGWTQEMRRERGLPIAL 238
 DB 181 RFTYLLPFSPTRLIEDTRYSDGDLDDGALAQAASLDYARRGWTQEMRRERGLPIAL 240
 QY 239 AHDAIGFMDHQAQAVPGAGLPHPTGYSLPYAAQVADATA--ARDLTASARRAVR 296
 DB 241 AHDAIGFMDHQAQAVPGAGLPHPTGYSLPYAAQVADAVAGISGPGTDALRGALR 300
 QY 297 GNAIDRADRDRLRLNRLFRGCPDRRYRLQRFYRLPOPLIERFYAGRLTLADRLRI 356
 DB 301 DYALDARDRFLRLNRLFRGCAPDRRYTLQRFYRPHGLIERFYAGRLSVADQLRI 360
 QY 357 VTGRPPILSQAVRCLPERPLQERA 382
 DB 361 VTGKPPILGTALRCLPERPLKENA 386
 RESULT 5
 AAW99096
 ID AAW99096 standard; protein; 386 AA.
 XX
 AC AAW99096;
 XX
 DT 14-MAY-1999 (first entry)
 XX
 DE Agrobacterium aurantiacum crtY protein sequence.
 XX
 KW Beta-carotene hydroxylase; crtY; crtB; crtE; crtI; xanthophyll;
 KW metabolite.
 XX
 OS Agrobacterium aurantiacum.
 XX
 PN JP1046770-A.
 XX

XX 23-FEB-1999.
XX
XX 07-AUG-1997; 97JP-00213648.
XX
XX 07-AUG-1997; 97JP-00213648.
XX
XX (KIRI) KIRIN BREWERY KK.
XX
XX WPI: 1999-208113/18.
XX N-PSDB; AAK19116.
XX
XX Beta-carotin hydroxylase - useful for preparation of xanthophylls and their metabolites.
XX
XX Disclosure; Page 9-11; 17pp; Japanese.
XX
XX The present invention describes beta-carotin hydroxylase. Beta-carotene
XX can be used in the preparation of xanthophylls and their metabolites. The
XX present sequence represents an Agrobacterium aurantiacum crtY protein
XX sequence from the present invention
XX
XX Sequence 386 AA;

Query Match 72.8%; Score 1456; DB 2; Length 386;
Best Local Similarity 71.8%; Pred. No. 1.1e-143;
Matches 277; Conservative 39; Mismatches 66; Indels 4; Gaps 2;

QY 1 MSHDLLIAGAGISGALIALAVRRDRDARIWLDARSGPSDOHTWSCHDTLSPFWLRL 60
DB 1 MTHDVILAGAGLANGLIALALRAARPDRLVLLDHAAGPSDGHWSCHDPLSPFWLRL 60
QY 61 SPIRGEWTDQEVAPFDDSRRLITGYSIEAGALIGLL--OGVDLRNTHVATLDDTGAT 118
DB 61 KPLRRANWPDQEVPRFRRARRLATYGSIDGALADAVRSGAEIRMSDIALDAQAT 120
QY 119 LTDGSRIEACVYIDARGAVERPHTLVGFQKFGVEIETDAPHGVERPMIMDAIVPQMDGY 178
DB 121 LSCGTRIEAGVLDGRGAPSRRLTVGFQKFGVEIETDRPHGVPRPMIMDAIVPQMDGY 180
QY 179 RTIYLLPSPFTRILLIEDTRYSDGDLDDGALAQSIDYARRGWGTQEMREREGILPIL 238
DB 181 RTIYLLPSPFTRILLIEDTRYSDGDLDDGALAQSIDYARRGWGTQEMREREGILPIL 240
QY 239 AHDAIGFMRDHAQAVPVGLAGLFPHTVGYSLPYAAQVADALIA--ARDLTASARRAVR 296
DB 241 AHDAIGFMRDHAQAVPVGLAGLFPHTVGYSLPYAAQVADALIA--ARDLTASARRAVR 300
QY 297 GWAIDRADRDRLRLNRLMFRGCPDRRYRLQRFYRLPQPLIERFYAGRLTLADRLRI 356
DB 301 DVAIDRADRDRLRLNRLMFRGCPDRRYRLQRFYRLPQPLIERFYAGRLTLADRLRI 360
QY 357 VTGRPPPIPSQAVRCLPERPLQERA 382
DB 361 VTGKPPPIPGTARCLPERPLKENA 386

RESULT 6
ADQ96834
ID ADQ96834 standard; protein; 648 AA.
XX
XX ADQ96834;
XX
XX 23-SEP-2004 (first entry)
XX
XX CrtWcrtY amino acid sequence.
XX
XX carotenoid; transgenic plant; overlapping extension PCR amplification;
XX PCR: crtB; crtY; crtW; crtZ; astaxanthin; carotene;
XX grain crop; vegetable; crtWcrtY.
XX
XX Unidentified.
XX

FN CN1380415-A.
XX
XX 20-NOV-2002.
XX
XX 06-APR-2001; 2001CN-00105878.
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XX 06-APR-2001; 2001CN-00105878.
XX
XX (SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.
XX
XX Yao Q, Peng R, Xiong A;
XX
XX WPI: 2003-230997/23.
XX N-PSDB; ADQ96833; ADQ96933.
XX
XX Synthesis of related gene for producing carotenoid in transgenic plant,
XX useful for improving quality of grain crops and vegetable.
XX
XX Claim 2; Page 1-2; 36pp; Chinese.

The present invention relates to a related gene for producing carotenoid
in transgenic plant. The invention utilizes an overlapping extension PCR
amplification process and uses six genes of crtB, crtY, crtW, crtY
and crtZ as templates to synthesise the related gene for synthesising
astaxanthin with plant preference code and can make a synthetic gene for
expression in a plant to produce the carotene substances of astaxanthin.
The synthetic gene can be used to improve the quality of grain crops and
vegetables. The present sequence represents a specifically claimed
crtWcrtY amino acid sequence, which is used in the exemplification of the
present invention.

Sequence 648 AA;

Query Match 70.3%; Score 1405; DB 7; Length 648;
Best Local Similarity 69.2%; Pred. No. 5.1e-138;
Matches 267; Conservative 43; Mismatches 72; Indels 4; Gaps 2;

QY 1 MSHDLLIAGAGISGALIALAVRRDRDARIWLDARSGPSDOHTWSCHDTLSPFWLRL 60
DB 263 MTHDVILAGAGLANGLIALALRAARPDRLVLLDHAAGPSDGHWSCHDPLSPFWLRL 322
QY 61 SPIRGEWTDQEVAPFDDSRRLITGYSIEAGALIGLL--OGVDLRNTHVATLDDTGAT 118
DB 323 KPLRRANWPDQEVPRFRRARRLATYGSIDGALADAVRSGAEIRMSDIALDAQAT 382
QY 119 LTDGSRIEACVYIDARGAVERPHTLVGFQKFGVEIETDAPHGVERPMIMDAIVPQMDGY 178
DB 383 LSCGTRIEAGVLDGRGAPSRRLTVGFQKFGVEIETDRPHGVPRPMIMDAIVPQMDGY 442
QY 179 RTIYLLPSPFTRILLIEDTRYSDGDLDDGALAQSIDYARRGWGTQEMREREGILPIL 238
DB 443 RTIYLLPSPFTRILLIEDTRYSDGDLDDGALAQSIDYARRGWGTQEMREREGILPIL 502
QY 239 AHDAIGFMRDHAQAVPVGLAGLFPHTVGYSLPYAAQVADALIA--ARDLTASARRAVR 296
DB 503 AHDAIGFMRDHAQAVPVGLAGLFPHTVGYSLPYAAQVADALIA--ARDLTASARRAVR 562
QY 297 GWAIDRADRDRLRLNRLMFRGCPDRRYRLQRFYRLPQPLIERFYAGRLTLADRLRI 356
DB 563 DVAIDRADRDRLRLNRLMFRGCPDRRYRLQRFYRLPQPLIERFYAGRLTLADRLRI 622
QY 357 VTGRPPPIPSQAVRCLPERPLQERA 382
DB 623 VTGKPPPIPGTARCLPERPLKENA 648

RESULT 7
ADP74123
ID ADP74123 standard; protein; 380 AA.
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XX ADP74123;
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XX 26-AUG-2004 (first entry)
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XX

XX XX Pantoea ananatis Crty.
XX XX
XX XX ketocarotenoid; ketolase; carotenoid; hydroxylase; beta-cyclase;
KW asexanthin; adonirubin; canthaxanthin; adoxanthin; zeaxanthin;
KW antioxidant; pigment; animal feed; trout; salmon; shrimp;
KW food supplement; enzyme.
XX
XX Pantoea ananatis.
OS
XX DE10253112-A1.
PN
XX 03-JUN-2004.
PD
XX 13-NOV-2002; 2002DE-01053112.
PE
XX 13-NOV-2002; 2002DE-01053112.
PR
XX 13-NOV-2002; 2002DE-01053112.
XX
XX (SUNG-) SUNGENE GMBH & CO KGAA.
PA
XX
PI Sauer M., Flachmann R., Klebsattel M., Schopfer CR;
DR WPI: 2004-489014/47.
XX N-PSDB; ADP74122.
XX
XX Production of ketocarotenoids with low hydroxylated by-product content,
PT for use e.g. in pigmenting feedstuffs, by culturing genetically modified
PT organisms having modified ketolase activity.
XX
XX Example 2; SEQ ID NO 25; 101pp; German.
XX
XX This invention describes a novel method for the production of
XX ketocarotenoids which involves culturing genetically modified organisms
CC having modified ketolase (KLA) activity. The starting microorganisms
CC produce carotenoids (naturally or by genetic supplementation), and are
CC specifically microorganisms (especially bacteria, yeasts, algae or fungi)
CC or plants. Microorganisms and plants involved in the method could include
CC Escherichia, Flavobacterium, Nostoc, Synechocystis, Hansenula, Fusarium,
CC Dunaliella, Rhodospirillum, Rhodospirillum rubrum, Rhodospirillum rubrum,
CC Solanaceae, Lamiaceae, Acacia, Calendula, Gentiana, Helianthus, Linum,
CC Rhododendron, Spartium and Zinnia. The modified microorganisms
CC additionally show elevated hydroxylase and/or beta-cyclase activity. The
CC ketocarotenoids described in the invention include asexanthin,
CC adonirubin, canthaxanthin, adoxanthin and zeaxanthin. Ketocarotenoids are
CC natural antioxidants and pigments, especially useful as pigmenting
CC additives in animal feed, specifically feed for trout, salmon or shrimps.
CC Ketocarotenoid-producing genetically modified organisms can be used as
CC feedstuffs or foodstuffs, in the production of ketocarotenoid-containing
CC extracts or for producing feed or food supplements. The process provides
CC large amounts of ketocarotenoids having a low content of hydroxylated by-
CC products, especially in the case of asexanthin, preferably due to
CC expression of at least one nucleic acid encoding hydroxylase and/or beta-
CC cyclase. DNA encoding the whole primary ketolase sequence from Nostoc sp.
CC strain PCC7120 was isolated, amplified by PCR and used to produce a
CC plasmid pNOSTR-G. A plasmid pMCL-Crt-Y1B2/IdI/gps, for the synthesis of
CC asexanthin in Escherichia coli, was constructed in 3 stages via the
CC intermediate stages pMCL-CrtY1B2 and pMCL-CrtY1B2/IdI, using the high
CC copy number plasmid vector pMCL200. Escherichia coli strain TOP10 was
CC transformed with the plasmids pNOSTR-G and pMCL-Crt-Y1B2/IdI/gps to give
CC carotenoid producing strain.
XX
XX Sequence 380 AA;
XX

Query Match	40.5%	Score 810.5	DB 8	Length 380
Best Local Similarity	45.6%	Pred. No. 6.5e-76		
Matches 171, Conservative	59	Mismatches 138	Indels 7	Gaps 4

[illegible]

Db 65 LVVHHMPDYQVNEPRTRKRLNSGVCILTSQGFAYELQRFQEPHLMMDTAVAEVAASSVRL 124

Qy 120 TDOSRLEAACVYDARGAVETPHLTGTFQKFTVGEIETDPAEGERVPMINDATTPQNDGTR 179

Db 125 KKQGVGAAPVADIGKRYAANSALSVGFQAFIQEORLSSHPIGGLSSPIMQATYQOOGYR 184

Qy 180 FYILPEPSEPTLIEBTRYSDGDDLDLALQASLDYANARGWTGQE-MRERESTLPAL 238

Db 185 FVYSLFSLSTPLRIEDTHYIDNATLDPBCAQONICDYAAQGGWQLOTLNEBQALPITL 244

Qy 239 AHAHIGFWMDHQAQAVPVGAGGLPHPTGYSLPAAQVADALAAIDL-TTASARAQVRG 297

Db 245 SGNAADFWQORPLAC--SGLRAGLPHPTTGYSLPAAVADARLSALDLPFVSASHHAITH 302

Qy 298 WATDRAADRDRFTLLINRMFLFRGCPDPRRYVLLQRFYLLPQPLIERFYAGRLTLADRLLIV 357

Db 303 FARERWQGGQFPRMLNRMFLAGPADSRMRVWQFPGYLEDLLIARFYAGKULTLDRRLT 362

Qy 358 TGRPPILPDAQVRL 372

Db 363 SGKEPVVITALQAI 377

RESULT 8
AAR07465
ID AAR07465 standard; protein; 382 AA

AC AAR07465 ;

DT	24-OCT-2003	(revised)
DT	28-JAN-1991	(first entry)

DE Polypeptide with enzymatic activity for the conversion of lycopene into
DE beta-carotene.

KW Carotenoid biosynthesis; vitamin A; cancer; food coloring

OS *Pantoea ananatis*.

PN EP393690-A.

PD 24-OCT-1990

PF 20-APR-1990; 90EP-00107493.

PR 21-APR-1989; 89JP-00103078.

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DR N-PSDB; AAQ06295.

PT DNA sequences encoding enzymes for carotenoid biosynthesis - for prodn.

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CC coloring, vitamin A precursor, and possibly in prevention of cancer. See **CAROTENES**.

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Best Local Similarity 45.6%; Pred. No. 6.6e-76;
Watched 171; Generated 50; Watched 120; Total 4

	MATCHES	1 / 1	CONSERVATIVE	39	MISMATCHES	136	INDEX	1	GAPS	4
OY	3	HDLIIAGAGSAGIATLAVNRDRRPDAITVMIDARSGPSDDTWSCHDTLSPEMLARISP	62							
		::::: ::: ::: ::: ::: ::: ::: ::: :::								
DG	5	YDILVLVAGLANGIATLARLOOQDPDMRLILLIDAAPQACGNNTWTFNHDDLTESQHRWLAP	64							

Oy		65	IRGEWTDGVAAPHDSRLTTGYGSIENGALIGLQ---	-GVLDLRMNHVATLDDTGATL	119
Db		65	LVVHHMEDYCVRPETRRKINSGYCFITTSQRFAEYLQFQGHLLMDTAAVAEVAESVRL		124
Oy		120	TDSRIEACVDIRGAVETPHLTVGFOKEVVEIETAPRCHVERPMTADATPQMONGYR		179
Db		125	KKGCVIGARAVIDGRGAANSALSVGFQFTGOERLSHPHGLSSPIIMDTVTDOONGYR		184
Oy		180	FITYLPESPTRILIEPTRYSDDGDDLDAQAASLDYAARGWTGOE--MRERGILPIAL		238
Db		185	FVYSLPSPTRLIIEDTHYINDNTDPEGARNICDYAAGQGWQTLTREEGALITTL		244
Oy		239	AHAIDIGWRDHAGCAVPVIGAGLEFHPTVGYSLPYAAPADAIALAARDL-TTASARRAVRG		297
Db		245	SGNADAFWQQRPAC--SGLRAGLFPHPTGYSLPLAVAVADRSLSDLVFTSASHIHAIITH		302
Oy		298	WAIDRADRDFFLLLRMLFRGCPPPRRKRILLQRTYRLPOLPIEFYAGRLTTLADRIRIV		357
Db		303	FARERRQQOQGFPMFLNRMLFLAGPADSRWRVQRFYGPEDLIAFYAGKTLLTDRLRIL		362
Oy		358	TGRPPIPLSQAVRCL	372	
Db		363	SGKPVEVLALQAI	377	

RESULT 9
AAW82258
ID AAW82258 standard; protein; 382 AA

XX	AAW82258;
AC	
XX	
DT	17-OCT-2003 (revised)
DT	16-JUL-1999 (first entry)
XX	
DE	C. utilis crty protein.
XX	
KW	HMG-CoA; 3-hydroxy-3-methylglutaryl coenzyme A reductase; crty; carotenoid.
XX	
OS	Pichia jadinii.
XX	
PN	JPI0248575-A.
XX	
PD	22-SEP-1998.
XX	
PF	12-MAR-1997; 97JP-00058012.
XX	
PR	12-MAR-1997; 97JP-00058012.
XX	
PA	(KIRI) KIRIN BREWERY KK.
XX	
DR	WPI; 1998-560727/48.
DR	N-PSDB; AAV73182.
XX	
PT	Gene useful for increase in carotenoid production - and preparation of carotenoid.
XX	
PS	Example 2; Fig 15-17; 54pp; Japanese.
XX	
CC	This invention describes a novel method for the preparation of carotenoids using genes and proteins isolated from Candida utilis. The invention specifically describes the isolation of a 3-hydroxy-3- methylglutaryl coenzyme A (HMG-CoA) reductase protein. This sequence represents the Candida utilis crty protein which is used in the method of the invention. (Updated on 17-OCT-2003 to standardise OS field)
XX	
XX	Sequence 382 AA;
XX	

Query Match	40.5%	Score 810.5;	DB 2;	Length 382;
Best Local Similarity	45.6%;	Pred. No. 6.6e-76;		
Matches 171; Conservative	59;	Mismatches 138;	Indels 7;	Gaps 4

```

Qy      HDLLIAGAGSGMLALAPRRPARIVMLDASSGPDQHTSCDTHSPWMLARLSP 62
Db      5 YDILITGAGLNGILNLRLOOQOPMRKILLIDAPRQAGNHTTFSFHDDLTDESQHRIR 64
Qy      63 IRGEWTDQVAPPDHSRRLTTGYGISEAGALIGLQ---GVDRMNTHVATLDDTGATL 119
Db      65 LVVHHNPDVQVAFPTRRKRTNGSGFCLTSQGFARVLTQGFQPHLMQDTAAVVAASVRL 124
Qy      120 TDGSRLEAACVIDARGAVETPHLTVGFQKFTVGEIETDAPRGVERPMIMQATVPQNDGYR 179
Db      125 KKQGVVGAQAVVIDGQYAAANSALISVGFQAFIQEORLUSHPHGSLSPIMQATVDOQNGYR 184
Qy      180 FYTLRFPSPRTLIEGTRYSDGSDLDGALQAQSLDYAARGWGTQGE-MRREGILPIAL 238
Db      185 FVYSLPSLSPRTLIEDTHYIDNATLDEPCARONICTYAAQOGMQLTLLKEBQGAEPITL 244
Qy      239 AHDAGIFWMDHAQGANVPVIGAGLGFHPRTGYSLPYAAQVADAAIARDL-TTASARAVRG 297
Db      245 SGNAADAFMOQRPLAC--SGIRAGLGFHPRTGYSLPYAAVADRLBALDVPFASGJHNAITH 302
Qy      298 WAIDRADRDRLRLNRLMFRGCPDRRYRLLORFYRLPOPLIRFPAGRLTLADRIRIV 357
Db      303 FAERWQOQGFPMILNRLMFLAGPADSRWRVQRFGEEDLIARFYAGKLTLLDRRLIL 362
Qy      358 TGRPPIPLSQAVRCL 372
Db      363 SGKRPVAVTAAALQAI 377

```

RESULT 10	.
AAW87891	
ID	AAW87891 standard; protein; 382 AA.

XX
AC AAW87891;

DT	17-OCT-2003 (revised)
DT	10-MAR-1999 (first entry)
XX	Protein encoded by the carotenoid biosynthesis gene <i>crtY</i>
DE	

KM Carotenoid biosynthesis; astaxanthin diglucoside; crtE gene; crtB gene;
KM crtI gene; adonixanthin-3'-glucoside; astaxanthin monoglucoside;
KM carotenoid glycoside; crtY gene; crtZ gene; crtW gene;
KM food additive.

XX Pantoea ananatis.
OS

XX JP10327865-A.
PN

XX 15-DEC-1998
PD

XX	29-MAY-1997;	97JP-00140460.
PF		

XX 29-MAY-1997; 97JP-00140460.
PR

XX
PA (KIRI) KIRIN BREWERY KK.

PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK
XX

DR WPI; 1999-099030/09.
DR N-PSDB; AAV84083.

XX New carotenoid glucoside(s) - used as food additives.
PT

XX
PS Disclosure; Page 22-23; 26pp; Japanese.

xx The present sequence represents a protein involved in carotenoid biosynthesis. The specification describes astaxanthin diglycosides and CC adonixanthin-3'-glycosides. The specification also describes a method for CC the preparation of a carotenoid glycoside, in which all, or part of, CC the carotenoid biosynthesis genes *cr1b*, *cr1b*, *cr1c*, *cr1d*, *cr1e* or *cr1f* CC are introduced to a microbe or plant and expressed. The transformed CC organism is cultured and astaxanthin diglycosides, adonixanthin-3'- CC glycosides, and/or astaxanthin monoglycosides are collected. The

XX Pantoea stewartii.
 OS
 XX
 PN WO2003016503-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 15-AUG-2002; 2002WO-US026647.
 XX
 PR 15-AUG-2001; 2001US-0312646P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Bzostowicz PC, Cheng Q, Picataggio SK, Rouviere PE;
 XX
 DR WPI; 2003-268323/26.
 DR N-PSDB; ACC44761.
 XX
 PT Novel nucleic acid molecule isolated from Pantoea stewartii encoding a
 PT carotenoid biosynthetic enzyme, useful for regulating carotenoid
 PT biosynthesis in an organism.
 XX
 PS Claim 4; Page 61-62; 68pp; English.
 XX
 CC The present invention describes Pantoea stewartii carotenoid biosynthetic
 CC enzymes (I). More specifically described are the geranylgeranyl
 CC pyrophosphate synthase (crts), zeaxanthin glucosyl transferase (crtx),
 CC lycopene cyclase (crtY), phytoene desaturase (crtI), phytoene synthase
 CC (crtB) and beta-carotene hydroxylase (crtZ) enzymes (see ABP96685 to
 CC ABP96690) encoded by ACC44759 to ACC44764. (I) can be used for regulating
 CC carotenoid biosynthesis in an organism, by over-expressing (I) in an
 CC organism, such that the carotenoid biosynthesis is altered in the
 CC organism. (I) and the genes encoding (I) are useful for converting
 CC phytoene to the carotenoids, for creating recombinant organisms that have
 CC the ability to produce various carotenoid compounds, and also for
 CC enhancing or manipulating carotenoid compounds. (I) can also be used for
 CC producing gene products having enhanced or altered activity
 XX
 SQ Sequence 382 AA;
 Query Match 39.2%; Score 783.5; DB 6; Length 382;
 Best Local Similarity 43.7%; Pred. No. 4.5e-73;
 Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps 6;
 QY 3 HDLLGAGLSGSLTAAVDRRPRDRIWLDARSGSDHTSCHDTDS---PEWLAR 59
 DB 5 YDILVAGAGLNGILALRIQQOQHPRKILLIEAGPEAGNHTWSFHEEDTTLNQHRITA- 63
 QY 60 LSPIRRGEMTDQVAFPPDHSRLTTGYSIEAGALIGLQ---GVDLRWNTHTVATLDDTG 116
 DB 64 --PLVVHHPDYVRFPORRRHNSGYTCSTRHFAILQQOQHMLHTAVSAVAHS 121
 QY 117 ATLTDSRIEACVIDARGAVETPHLTVGQKEVGEIETDAPHGVPERMINDATVPQMD 176
 DB 122 VQADGRITIASIVIDRGYTPDSALRVGFQAFIQGEMQASAHGSSPIMDATVQDN 181
 QY 177 GYRFITLPPSPRRIIEEDTRYDGDLDGALAAQSLDYAARGWTGDE-WREREGILP 235
 DB 182 GRAFVYTLPLSAPALIEDTHYIDKANTQARARONIRDYAAQGWPLQTLAEEBOGALP 241
 QY 236 IALAHAIIGFWRHAGAAVAVGLAGLFHPTGYSLPYAAQVADATAAARDL-TTASARRA 294
 DB 242 ITLTGNRQFWQOQPOAC--SGIRAGLFFHTTGYSLPLAVALDRLSALDVFFSSSVHQT 299
 QY 295 VRCMAIDRADRDREFLRLNMLFRGCPDRRYRLRFRYRLPOLIERFYAGRLTLADRI 354
 DB 300 IAHFAQOQWQOQGFPRNLNMLFLAGPABSRWVRWQRFYGLPBDLLARFYAGRLTYTDLR 359
 QY 355 RIYTGRRPIPLSQAVRCL 372
 DB 360 RIISGRPPVPVFAALAI 377

RESULT 15
 ADQ14629
 ID ADQ14629 standard; protein; 382 AA.
 XX
 AC ADQ14629;
 XX
 DT 23-SEP-2004 (first entry).
 XX
 DE Pantoea stewartii lycopene cyclase SEQ ID NO:6.
 XX
 KW carotenoid, carotenoid overproducing microorganism;
 KW functional isoprenoid enzymatic biosynthetic pathway; Pantoea stewartii;
 KW crtY; lycopene cyclase; enzyme.
 XX
 OS Pantoea stewartii.
 XX
 PN WO2004056974-A2.
 XX
 PD 08-JUL-2004.
 XX
 PF 19-DEC-2003; 2003WO-US041811.
 XX
 PR 19-DEC-2002; 2002US-0435612P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cheng Q, Rouviere PE, Tao L;
 XX
 DR WPI; 2004-525436/50.
 DR N-PSDB; ADQ14628.
 XX
 PT Novel carotenoid overproducing microorganism comprising genes encoding
 PT functional isoprenoid enzymatic biosynthetic pathway comprising disrupted
 PT genes such as dead, mtec, and yfhe, useful for producing carotenoid.
 XX
 PS Example 2; SEQ ID NO 6; 85pp; English.
 XX
 CC The present invention describes a carotenoid overproducing microorganism
 CC comprising the genes encoding a functional isoprenoid enzymatic
 CC biosynthetic pathway comprising a disrupted gene chosen from dead, mtec,
 CC and yfhe. Also described is a carotenoid overproducing Escherichia coli
 CC microorganism (II) comprising an upper isoprenoid enzymatic biosynthetic
 CC pathway comprising the genes dxs, dxr ygbP, ycbB, ygbB, lylB, lyl, lspa
 CC and lspb, a lower isoprenoid enzymatic biosynthetic pathway comprising
 CC the genes crtE, crtB, crtI, and crtY, mutations chosen from a mutation in
 CC the thrs gene of the 3159 nucleotide sequence of SEQ ID NO:35 (ADQ14658),
 CC mutation in the rpsA gene of the 2904 nucleotide sequence of SEQ ID NO:37
 CC (ADQ14660), mutation in the rpoC gene of the 5454 nucleotide sequence of
 CC SEQ ID NO:38 (ADQ14661), mutation in the yfhe gene of the 1845 nucleotide
 CC sequence of SEQ ID NO:39 (ADQ14662), or mutation in the rhol gene of the
 CC 2676 nucleotide sequence of SEQ ID NO:41 (ADQ14664), where the genes of
 CC the lower isoprenoid enzymatic biosynthetic pathway reside on an
 CC autonomously replicating plasmid comprising a replicon chosen from p15A
 CC and pMB1. (I) chosen from bacteria, yeasts and filamentous fungi such as
 CC Achromobacter, Trichoderma, Saccharomyces, Pichia, Candida, Hansenula,
 CC Salmonella, Bacillus, Acinetobacter, Zymomonas, Agrobacterium,
 CC Erythrobacter, Chlorobium, Chromatium, Flavobacterium, Cytophaga,
 CC Rhodospirillum rubrum, Rhodococcus, Streptomyces, Brevibacterium, Corynebacteria,
 CC Mycobacterium, Deinococcus, Paracoccus, Escherichia, E. coli, Pantoea,
 CC Pseudomonas, Sphingomonas, Methylobacter, Methylobacter, Methylobacter,
 CC Methylobacter, Methylobacter, Methylobacter, Alcaligenes,
 CC Synecoccus, Synecoccus, Anabaena, Thiobacillus thioautotrophicus,
 CC Methanobacterium, Klebsiella, and Myxococcus, and (II) are useful for
 CC producing carotenoid which involves contacting (I) or (II) with a
 CC fermentable carbon substrate, growing the carotenoid overproducing
 CC microorganism for a sufficient time to produce carotenoid, and optionally
 CC recovering the carotenoid from the carotenoid overproducing
 CC microorganism. The present invention represents Pantoea stewartii lycopene
 CC cyclase which is encoded by the crtY gene, and is used in an example from
 CC the present invention.
 XX
 SQ Sequence 382 AA;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 19:42:50 ; Search time 4528.7 Seconds

(without alignments)
9657.484 Million cell updates/sec

Title: US-10-695-980-1_COPY_5794_6942

Perfect score: 1149

Sequence: 1 tcatgctcctcctcgcagca.....atccagcagatcatgctcat 1149

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_gsat1:*
9: gb_gsat2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	81.4	7.1	1180	9	CL513526 SAIL_876
C 2	75.4	6.6	1798	9	AG171124 Pan trogl
C 3	75.2	6.5	932	9	CNS00720
C 4	73	6.4	1577	7	CK419311 ANF IPova
C 5	72.6	6.3	1278	9	AG060116 Pan trogl
C 6	71	6.2	1798	9	AG171124 Pan trogl
C 7	70.6	6.1	935	9	CNS006XK
C 8	70	6.1	1821	9	CL090850
C 9	69.8	6.1	1189	9	AG030608 Pan trogl
C 10	69.6	6.1	1406	9	CG756569 P051-4-80
C 11	69	6.0	938	9	AG036223 Pan trogl
C 12	69	6.0	1090	6	CA790876 AGENCOURT
C 13	68.2	5.9	929	9	CL501227 SAIL_694
C 14	68	5.9	896	9	AG159205 Pan trogl
C 15	68	5.9	1250	9	AG043469 Pan trogl
C 16	67.6	5.9	925	9	CNS0091P
C 17	67.6	5.9	1057	9	CNS04680
C 18	67.6	5.9	1348	9	CG752544 P047-2-C1
C 19	67.4	5.9	1375	2	AW727483 RA_Ra001
C 20	67.4	5.9	1448	8	CC194731 CH261-183
C 21	67.4	5.9	2193	9	CL469745 SAIL_133
C 22	67.2	5.8	1216	9	AG441574 Mus muscu
C 23	67.2	5.8	1309	9	AG077201 Pan trogl
C 24	66.2	5.8	1244	4	BG846745 1024014HO

25	66.2	5.8	1413	9	CL505027 SAIL_744
C 26	66.2	5.8	2332	9	AG363333 Mus muscu
C 27	65.6	5.7	1244	4	BG846745 1024014HO
C 28	65.4	5.7	633	9	AG043206 Pan trogl
C 29	65.4	5.7	932	9	CNS00720
C 30	65.2	5.7	1037	9	AG061836 Pan trogl
C 31	65.2	5.7	1100	9	CNS0168D
C 32	65.2	5.7	1821	9	CL090560 ISB1-17N1
C 33	64.6	5.6	467	9	CG058960 PUFWD21TB
C 34	64.6	5.6	654	8	CC438940 PUFWD22TD
C 35	64.6	5.6	667	9	CG414823 PUFWD21TB
C 36	64.6	5.6	733	8	BZ989278 PUFWD20TB
C 37	64.6	5.6	883	8	CC401856 PUFWD26TD
C 38	64.6	5.6	902	9	CG121335 PUFWD48TB
C 39	64.6	5.6	914	8	CC378162 PUFWD81TD
C 40	64.6	5.6	923	9	CG327267 OG0FL78TV
C 41	64.6	5.6	983	8	CC387908 PUFWD62TD
C 42	64.6	5.6	1341	9	AG030611 Pan trogl
C 43	64.2	5.6	925	9	CNS0091P
C 44	64	5.6	1462	9	AG441877 Mus muscu
C 45	64	5.6	1538	9	AG030607 Pan trogl

ALIGNMENTS

RESULT 1
CL513526 1180 bp DNA linear GSS 01-APR-2004
LOCUS SAIL_876_G03.v2 SAIL Collection Arabidopsis thaliana genomic clone
DEFINITION SAIL_876_G03.v2, genomic survey sequence.
ACCESSION CL513526
VERSION CL513526.1 GI:46010846
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 1180)

Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutcheson,D., Kimerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
A high-throughput Arabidopsis reverse genetics system

TITLE

JOURNAL
MEDLINE
PUBMED

COMMENT

Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS839448; T-DNA left border flanking sequences of
through the Arabidopsis Insertion library (SAIL) lines are available
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.

FEATURES

source

1..1180
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL_876_G03.v2"
/clone.lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN

Query Match 7.1%; Score 81.4; DB 9; Length 1180;
Best local Similarity 44.9%; Pred. No. 4,2e-07;

QY 128 TCGATCAGCGCTGCGGAGCGGTAGAAACCGCTGACGACGAGCGATGCGCGTGGC 187
Db 1013 GCGCGGCGGCG 954
QY 188 GGGCAGCGCGGAGACGACATCCGCTTCAGACGCGGAGGAGCGGTGCGGATCCGCGCA 247
Db 953 CCGGCG 894
QY 248 TCGATGCG 304
Db 893 NCG 835
QY 305 GCGATGCGCATCCGCGACCTGCGCGCGCATAGGAGCGAGCAATATCCGCTGACGCGGTGAAAC 364
Db 834 GCG 775
QY 365 AGCGCTGCG 417
Db 774 CCG 715
QY 418 GCGTATGCGGTATAGGCGCGCGCGCGCATGCGCGCGCGCGCGCGCGCGCGCGCGCG 477
Db 714 CCG 655
QY 478 CCGCGTCAAGCGCGCGCGCGCGCGCATAGTCAAGCGACGCGCTGCGCGCGCGCGCATGTC 537
Db 654 CCG 595
QY 538 CAGATGCG 563
Db 594 CCG 569

RESULT 6
AG171124/c 1798 bp DNA linear GSS 09-JAN-2002
LOCUS Pan troglodytes DNA, clone: RPA3-040F09.TJ, genomic survey
DEFINITION sequence.
ACCESSION AG171124
VERSION AG171124.1 GI:1670802
KEYWORDS
SOURCE Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
TITLE Totsuki, Y., Watanabe, H. and Sakaki, Y.
JOURNAL BAC end sequences of library RPCI-43
REFERENCE Unpublished
AUTHORS
TITLE 2 (bases 1 to 1798)
JOURNAL Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totsuki, Y., Watanabe, H. and Sakaki, Y.
DIRECT SUBMISSION
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9111, Fax: 81-45-503-9170
E-mail: chimpesegsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

COMMENT
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
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/db_xref="taxon:9598"

FEATURES
source

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Matches 463; Conservative 0; Mismatches 644; Indels 21; Gaps 5;
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/sex="male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC library"

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QY 62 ATGGCG 121
Db 1658 GNGCG 1599
QY 122 AAGCGCTGATCAGCG 181
Db 1598 CCG 1545
QY 182 TCGGCG 241
Db 1544 NGGCG 1485
QY 242 GCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
Db 1484 GCG 1425
QY 302 GCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 361
Db 1424 NCG 1365
QY 362 AACGCGCTGCG 421
Db 1364 CCG 1305
QY 422 ATGGCGTATGCG 481
Db 1304 GNGCG 1245
QY 482 GTCAGCG 541
Db 1244 CCG 1188
QY 542 TCG 601
Db 1187 CCG 1128
QY 602 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
Db 1127 GCG 1068
QY 662 TCGAGCG 721
Db 1067 GCG 1008
QY 722 GTCAAGTGGGCGGTCTGCAACGACCGAGCGGTGATGATGATGATGATGATGATGAT 781
Db 1007 GCG 948
QY 782 GAGCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 841
Db 947 GCG 892
QY 842 AGATGACACCTGAGAGCG 901
Db 891 GCG 839
QY 902 GTCAAGCG 961
Db 838 CCG 779

Oy	962	ATGGGCGCAGACGCGCCAGCATTCGGGCGGAAGAATCGGTGTGTGCAGAGCAAGTGTG	1027
Dd	778	GCGNCGGCGCGCGCGNCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	720
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Dd	719	CG	660
Oy	1082	TCGGGAAGCGCAAGCGCATCAAGCGCACCGGACAGCCCCCGGCCCGCGG	1129
Dd	659	CCG	612
RESULT 7			
CMS006XK/c			
LOCUS			
Drosophila melanogaster genome survey sequence T7 end of BAC #			
DEFINITION			
BACR14N09 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION			
AL066051			
VERSION			
AL066051.1 GI:4945019			
KEYWORDS			
GSS.			
SOURCE			
Drosophila melanogaster (fruit fly)			
ORGANISM			
Drosophila melanogaster			
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
Ephydroidea; Drosophilidae; Drosophila.			
REFERENCE			
1 (bases 1 to 935)			
AUTHORS			
Genoscope.			
JOURNAL			
Direct Submission			
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefegenoscope.cns.fr			
COMMENT			
Web : www.genoscope.cns.fr)			
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPl-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.			
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Matches 130; Conservative 98; Mismatches 176; Indels 1; Gaps 1			
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Dd	930	GGGGSGSSSGSSGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	871
Oy	291	TCAGGTGCGCGCGCGCATGTGCGCGACTTGCGCGCGCATATGGCGAGCAATATCCGG	350
Dd	870	GCSGCGSCGGS CCS CGCGCGSGSSGCGGCCGCGGCCGCGGSCGCGSCGCGCGCG	811
Oy	351	TGAGC-GGGTGAACGCTTGTCCCGCCCAAGCCCAACCGGACCGCCCGCTGTGCGTGTG	409

[illegible]

KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 1406)
AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Bunjer,J., van der Meulen,M. and Sommer,R.J.
TITLE An integrated physical and genetic map of the nematode Pristionchus
pacificus
JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)
MEDLINE 22835951
PUBMED 12884007
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

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/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

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Query Match 6.1%; Score 69.6; DB 9; Length 1406;
Best Local Similarity 44.6%; Pred. No. 0.00014;
Matches 424; Conservative 0; Mismatches 518; Indels 9; Gaps 4;
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294 CCGGCG 353
239 TCCGCGCGATGATGAGCG 298
354 CCG 413
299 CCG 358
414 CCG 473
359 TGGAAAGCG 418
474 GAGCG 533
419 CCTATGCGCTATGAGCG 478
534 GCG 591
479 CCGGTTCCAGCCCG 538
592 CCG 651
539 AGATCG 598
652 GCG 711
599 ACGAGATGATGAAGCGGTACCGGTTCATCTCGATCGGAAACGCGCGGTCTCATATCGAG 658
712 GCG 766
659 CGCTGACGCGCATGGGGGCGGTCTGATCTGACGCCACGAATTTCTGAAAACCC 718
767 CCG 826

QY 719 ACGGTCAAGTG-CGGGTTCTGACGCGACCAACGCGCGCTTCATCAACGAGAGCCTCGAT 777
DB 827 CCG 886
QY 778 CCGGAGCG 837
DB 887 CCG 946
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DB 947 GCGGCG 1006
QY 898 TGTCTGTCAGCG 957
DB 1007 CCNCG 1065
QY 958 ACGATGGGCGCAAGCG 1017
DB 1066 GCG 1125
QY 1018 GGTGTGTCGTTCGAGGCG 1077
DB 1126 CCG 1185
QY 1078 GCGGTGCGGAACGCGCAACCGCGATACGCGCACCGGACGCGCGCGCGCGCGCGCGCG 1128
DB 1186 CCGGCG 1236

RESULT 11
LOCUS AG036223 938 bp DNA linear GSS 01-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-012B18.F, genomic survey sequence.
ACCESSION AG036223
VERSION AG036223.1 GI:16563096
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 938)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
E-mail:chimbese@sc.riken.go.jp, URL:http://npg.gsc.riken.go.jp/
Tel:81-45-503-9111, Fax:81-45-503-9170
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RAD process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
location/Qualifiers
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/sex="male"
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/clone_lib="PTB Chimpanzee Male BAC library"

ORIGIN

Bullis, D., Snell, J., Miguel, T., Hutcheson, D., Kimmerly, B.,
Mitzel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S. A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

12468722

Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com

ABRC Stock Number CS830561: T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: T-DNA tagged.

FEATURES
source

1..929
location/Qualifiers
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/db_xref="taxon:3702"
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/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN

Query Match 5.9%; Score 68.2; DB 9; Length 929;
Best Local Similarity 47.9%; Pred. No. 0.0028;
Matches 210; Conservative 0; Mismatches 227; Indels 1; Gaps 1;

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DB 407 GGG 466
QY 117 CATGAAGCGCTGATCAGCGGCTGCGGCGAGCGGCTGAACCGCTGACAGCAGCGCATAGC 176
DB 467 GGG 526
QY 177 GACGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 236
DB 527 GGG 586
QY 227 GATCGCGCGATGATGCG 296
DB 587 GCG 646
QY 297 CGCGCGCGCGATGCGATCGCGACCTGCGCGCATAGGCGAGCGAATATTCGATGACG 356
DB 647 GGG 706
QY 357 GGTGAACAAGCCCTGCG 416
DB 707 GCG 765
QY 417 AGCTATGCGCTATGCG 476
DB 766 CCG 825
QY 477 GCCCGATCCAGCCCGCC 494
DB 826 GCCG 843

RESULT 14

AG159205/1
LOCUS AG159205 896 bp DNA linear GSS 09-JAN-2002
DEFINITION Pan troglodytes DNA, clone: RP43-024K15.T7, genomic survey
ACCESSION AG159205
VERSION AG159205.1 GI:1668883

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
REFERENCE
AUTHORS
TITLE
JOURNAL

GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library RPCT-43
Unpublished
2 (bases 1 to 896)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@sc.riken.go.jp, url: http://ngp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCT-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
location/Qualifiers
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FEATURES
source

Query Match 5.9%; Score 68; DB 9; Length 896;
Best Local Similarity 47.3%; Pred. No. 0.0003;
Matches 259; Conservative 0; Mismatches 286; Indels 3; Gaps 2;

ORIGIN

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DB 844 GCG 785
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DB 784 CCG 725
QY 125 CGCTGATCAGCGGCTGCGGAGCG--GGTGAACCGCTGAGCAGCGATAGCAGCGT 182
DB 724 GCG 665
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DB 183 CCG 242
QY 664 GCG 605
DB 243 CGCGATGATGCG 301
QY 604 GGGGGCG 545
DB 302 GCCCGATGCGATCCGCGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 361
QY 544 GCG 485
DB 362 AACAGCCCTGCG 421
QY 484 GCG 425
DB 422 ATGGCTATGAGGCG 481

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 22:57:55 ; Search time 826.57 Seconds

(without alignments)
8628.994 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6054689 seqs, 3103772919 residues 12109378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1149	100.0	11233	10	US-09-920-923-27
5	1149	100.0	11233	18	US-10-695-980-27
6	248.8	21.7	1164	21	US-10-810-733-7
7	248.8	21.7	9127	21	US-10-810-733-20

C 8	236.4	20.6	1185	14	US-10-166-037-2
C 9	228.6	19.9	1170	20	US-10-808-807-5
C 10	228.6	19.9	5632	22	US-10-997-844-6
C 11	228.6	19.9	8814	20	US-10-808-807-18
C 12	228.6	19.9	8814	22	US-10-997-844-11
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C 17	209.8	18.3	1149	15	US-10-218-118-5
C 18	209.8	18.3	1149	18	US-10-363-567-29
C 19	209.8	18.3	1149	18	US-10-466-656-3
C 20	209.8	18.3	1149	19	US-10-735-019-5
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C 22	209.8	18.3	1149	20	US-10-735-442-5
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C 35	65	5.7	125401	19	US-10-203-295-35
C 36	64.6	5.6	2209	18	US-10-425-114-23000
C 37	64.4	5.6	1041	19	US-10-425-963-8597
C 38	63.2	5.5	2265	18	US-10-425-114-26996
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C 42	60	5.2	2392	17	US-10-369-493-31508
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C 44	59.2	5.2	1684	19	US-10-437-963-81995
C 45	59.2	5.2	1998	9	US-09-813-467-1

ALIGNMENTS

RESULT 1
US-09-547-267-8/C
Sequence 8, Appli
Patent No. US20020147371A1
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Teasler, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:


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QY 361 GAAACAGCCCTGCCCCCAAGCCCAACCGGACACCGCCCCCTGCGGTGTGCGCCAGAAAGCC 420
Db 6154 GAAACAGCCCTGCCCCCAAGCCCAACCGGACACCGCCCCCTGCGGTGTGCGCCAGAAAGCC 6213
QY 421 TATGGCGTATGAGCGAGCGATGAGGAGCAGATGCCCCCTTTGCGCGCGCATCTCTGCCC 480
Db 6214 TATGGCGTATGAGCGAGCGATGAGGAGCAGATGCCCCCTTTGCGCGCGCATCTCTGCCC 6273
QY 481 GGTTCAGCCCCGCTTGCGCGCATATGTCAGGACACGCTTGCGCGCAAGCGCCATCTGTCAG 540
Db 6274 GGTTCAGCCCCGCTTGCGCGCATATGTCAGGACACGCTTGCGCGCAAGCGCCATCTGTCAG 6333
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Db 6334 ATCCGCGCGCTGCTGTACCGGTATCTTCGATCAGAGAGCGGGTGGGACTGAAGGACAG 6393
QY 601 CAGATGATGAGAGCGGTACCCGTCATCTGCGGAAACGTCGCGTCATGATCATCGAGCG 660
Db 6394 CAGATGATGAGAGCGGTACCCGTCATCTGCGGAAACGTCGCGTCATGATCATCGAGCG 6453
QY 661 CTGACGCGCATGAGGAGCGTCTGCTCTGATCTGACGCGCCAGAAATTTCTGGAACCCAC 720
Db 6454 CTGACGCGCATGAGGAGCGTCTGCTCTGATCTGACGCGCCAGAAATTTCTGGAACCCAC 6513
QY 721 GGTCAAGTGGGGGTCTTCAACGCGACACAGGCGTGTGATCAGCAGGAGCGCTTCATCCG 780
Db 6514 GGTCAAGTGGGGGTCTTCAACGCGACACAGGCGTGTGATCAGCAGGAGCGCTTCATCCG 6573
QY 781 CGAGCGGTGCGTCAAGCGTGCAGCGCGCGGTATCTGTCAGCGCTGCGCAATGCGTTCACCG 840
Db 6574 CGAGCGGTGCGTCAAGCGTGCAGCGCGCGGTATCTGTCAGCGCTGCGCAATGCGTTCACCG 6633
QY 841 CAGATGACACCCCTGACGACGCCCATGACGCGCGCGCTTCGATGACCATTAAGCTGT 900
Db 6634 CAGATGACACCCCTGACGACGCCCATGACGCGCGCGCTTCGATGACCATTAAGCTGT 6693
QY 901 CGTCAAGCGCGCGCATGCTGCGGAAACCGCGACCTCTGATCCGTCATCTTCGCGCGAG 960
Db 6694 CGTCAAGCGCGCGCATGCTGCGGAAACCGCGACCTCTGATCCGTCATCTTCGCGCGAG 6753
QY 961 AATGGCGCAGAGCGCGCGCATTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
Db 6754 AATGGCGCAGAGCGCGCGCATTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6813
QY 1021 GTGCTGTGTCGAGGCGCGCGACCGCGCGCTGAGCATCAGATGCGCGCATCCGCTGCG 1080
Db 6814 GTGCTGTGTCGAGGCGCGCGACCGCGCGCTGAGCATCAGATGCGCGCATCCGCTGCG 6873
QY 1081 GTTCGCAACGCGCAAGCGCGCATGAGCGCACCGGACAGCCCCCGCGCGCATCAGCAGATC 1140
Db 6874 GTTCGCAACGCGCAAGCGCGCATGAGCGCACCGGACAGCCCCCGCGCGCATCAGCAGATC 6933
QY 1141 ATGGCTCAT 1149
Db 6934 ATGGCTCAT 6942
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RESULT 4

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US-09-920-923-27
; Sequence 27, Application US/09920923
; Publication No. US2003002273A1
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tsyanikov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/09/920,923
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; PRIOR FILING DATE: 1997-12-01
```

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; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11233
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Plasmid pze4
US-09-920-923-27

Query Match 100.0%; Score 1149; DB 10; Length 11233;
Best Local Similarity 100.0%; Pred. No. 8,2e-282; Mismatches 0; Indels 0; Gaps 0;
Matches 1149; Conservative

QY 1 TCATGCTCTCTCTGACAGAGGAGCGTTCGAGGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 60
Db 6476 TCATGCTCTCTCTGACAGAGGAGCGTTCGAGGAGGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 6535
QY 61 AATGGCGCGCGCGTCCGATGACGATGCGAAGCCGATCGGCGCAATGTCAAGCGCGCGCGCATYA 120
Db 6536 AATGGCGCGCGCGTCCGATGACGATGCGAAGCCGATCGGCGCAATGTCAAGCGCGCGCGCATYA 6595
QY 121 GAAGCGCTGATCAGCGCGCTGCGAGCGCGGTGAAGCCGCTGACAGCAGGCGATGACGACG 180
Db 6596 GAAGCGCTGATCAGCGCGCTGCGAGCGCGGTGAAGCCGCTGACAGCAGGCGATGACGACG 6655
QY 181 GTGCGGCGGAGCGCGGGAACAGCATCGGTTGACGCGCGCGAGAGCGGATCGTCAGATC 240
Db 6656 GTGCGGCGGAGCGCGGGAACAGCATCGGTTGACGCGCGCGAGAGCGGATCGTCAGATC 6715
QY 241 CGCGCGATGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 6716 CGCGCGATGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6775
QY 301 CGCGCGATGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 6776 CGCGCGATGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6835
QY 361 GAAACAGCCCTGCCCCCAAGCCCAACCGGACACCGCCCCCTGCGGTGTGCGCCAGAAAGCC 420
Db 6836 GAAACAGCCCTGCCCCCAAGCCCAACCGGACACCGCCCCCTGCGGTGTGCGCCAGAAAGCC 6895
QY 421 TATGGCGTATGAGCGCGCGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
Db 6896 TATGGCGTATGAGCGCGCGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6955
QY 481 GGTTCAGCCCCGCTTGCGCGCATATGTCAGGACACGCTTGCGCGCGCGCGCGCGCGCGCAT 540
Db 6956 GGTTCAGCCCCGCTTGCGCGCATATGTCAGGACACGCTTGCGCGCGCGCGCGCGCGCGCAT 7015
QY 541 ATCCGCGCGGTGCTGTACCGGTATCTTCGATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Db 7016 ATCCGCGCGGTGCTGTACCGGTATCTTCGATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 7075
QY 601 CAGATGATGAGAGCGGTACCCGTCATCTGCGGAAACGATGCGCGTCATGATCATCGAGCG 660
Db 7076 CAGATGATGAGAGCGGTACCCGTCATCTGCGGAAACGATGCGCGTCATGATCATCGAGCG 7135
QY 661 CTGACGCGCATGAGGAGCGTGTGATCTGATCTGACGCGCGCGCAATTTCTGGAACCCAC 720
Db 7136 CTGACGCGCATGAGGAGCGTGTGATCTGATCTGACGCGCGCGCAATTTCTGGAACCCAC 7195
QY 721 GGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 7196 GGTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7255
QY 781 CGAGCGCTCGGTCAGCGCGTGCAGGATGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db 7256 CGAGCGCTCGGTCAGCGCGTGCAGGATGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 7315
QY 841 CAGATGACACCCCTGACGACGCCCATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 7316 CAGATGACACCCCTGACGACGCCCATGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7375
```

Qy	901	CGTCAGGCGGGCCGAATGTCGGGAAAGCGACCTCTCGATCCGTCAATTGGCGGACG	960
Qy	901	CGTCAGGCGGGCCGAATGTCGGGAAAGCGACCTCTCGATCCGTCAATTGGCGGACG	960
Db	7316	CGTCAGGCGGGCCGAATGTCGGGAAAGCGACCTCTCGATCCGTCAATTGGCGGACG	7435
Qy	961	AATGGGCGACAGCGCGCCAGCCATTTCGGGCGAAAGATCCGTGTCTGTGGCAGGACAGGT	1020
Db	7436	AATGGGCGACAGCGCGCCAGCCATTTCGGGCGAAAGATCCGTGTCTGTGGCAGGACAGGT	7495
Qy	1021	GTGCTGTGTCCGAGGGGCCGGAACCCGCGCTCGAGATCTCAATTTGGCGGATCCGATCTGCG	1080
Db	7496	GTGCTGTGTCCGAGGGGCCGGAACCCGCGCTCGAGATCTCAATTTGGCGGATCCGATCTGCG	7555
Qy	1081	GTCCGGAACCGGCAAGCGCGATTCAGCGCACTCGGACAGCCCGCGCCGCGATTCAGCAGATC	1140
Db	7556	GTCCGGAACCGGCAAGCGCGATTCAGCGCACTCGGACAGCCCGCGCCGCGATTCAGCAGATC	7615
Qy	1141	ATGGCTCAT 1149	
Db	7616	ATGGCTCAT 7624	

RESULT 5
US-10-695-980-27
Sequence 27, Application US/10685980
Publication No. US20040058410A1
GENERAL INFORMATION:
APPLICANT: Paesamontes, Luis
APPLICANT: Teygankov, Yuri
TITLE OF INVENTION: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C98435/125944)
CURRENT APPLICATION NUMBER: US/10/695,980
PRIOR FILING DATE: 2003-10-29
PRIOR APPLICATION NUMBER: US/09/920,923B
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 11233
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Plasmid pZea4
US-10-695-980-27

Query Match	100.0%	Score 1149;	DB 18;	Length 11233;
Best Local Similarity	100.0%;	Pred. NO. 8.2e-282;		
Matches 1149; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	TCATGCTCTCTCCCTGCAACAGAGGGGCGTTTCGGGCGAGGAGAGGCGACCGGCTTGGCAACAGCGG	60
Db	6476	TCATGCTCTCTCTCTGCAAGAGGGGCGTTTCGGGCGAGGAGAGGCGACCGGCTTGGCAACAGCGG	6535
Qy	61	AATGGGCGGGCGGTCCGGGTGACGATGCGAAGCCGGTCCGACATGTACAGCGCCCGGCATTA	120
Db	6536	AATGGGCGGGCGGTCCGGGTGACGATGCGAAGCCGGTCCGACATGTACAGCGCCCGGCATTA	6595
Qy	121	GAAAGCGCTCGATCAGCGGCTCGCGAGGCGGTGAACCCGTTGCAGACAGGCGATTAGCGAGC	180
Db	6596	GAAAGCGCTCGATCAGCGGCTCGCGAGGCGGTGAACCCGTTGCAGACAGGCGATTAGCGAGC	6655
Qy	181	GTCCGGCGGGCGAGCCGCGGGAACAGATCCGGTTTACGACGCCGCGAAGCGCGTGGCGATC	240
Db	6656	GTCCGGCGGGCGAGCCGCGGGAACAGATCCGGTTTACGACGCCGCGAAGCGCGTGGCGATC	6715
Qy	241	CGCGGATCGATGAGCCCAAGCCGCGCACCCGCGGACCGGCGCGCGGTCTCAGAGTCGCG	300
Db	6716	CGCGGATCGATGAGCCCAAGCCGCGCACCCGCGGACCGGCGCGCGGTCTCAGAGTCGCG	6775
Qy	301	CGCGGCGATGCGATCCGCGACCTTGCGCGGCAATAGGCGACGCGAATATCCGGTTGACGGGGTG	360

Db	6776	GGCCGCAGTGGCAATCCGGACCTTGCGCGGCATAGGGGACGAAATACCGGTGACGGGGTG	6835
OY	361	GAACAGCCCTTGTCCCTCCAGCCCAACCGGACATCGGCCCTTGGCGGTGTGGCGCCAGAAAGCC	420
Db	6836	GAACAGGCCCTTGTCCCTCCAGCCCAACCGGACATCGGCCCTTGGCGGTGTGGCGCCAGAAAGCC	6895
OY	421	TATGACGTCAATGGGACAGCGCGGATGGGACAGGATGCCCTTTCGGCGCGCATCTCTGCGC	480
Db	6896	TATGGCGTCAATGGGACAGCGCGGATGGGACAGGATGCCCTTTCGGCGCGCATCTCTGCGC	6955
OY	481	GGTCCAGCCCGCGCTGGCGGAGTATGATCAAGGACGCTTGGCGCAAGCGCGCATCTGTCCAG	540
Db	6956	GGTCCAGCCCGCGCTGGCGGAGTATGATCAAGGACGCTTGGCGCAAGCGCGCATCTGTCCAG	7015
OY	541	ATGCGCCCGCGGTGTGATAGCGCGGATCTCTGATCATAGATGGCGGGATGGGACCTGAAGGGGAG	600
Db	7016	ATGCGCCCGCGGTGTGATAGCGCGGATCTCTGATCATAGATGGCGGGATGGGACCTGAAGGGGAG	7075
OY	601	CAGATAGATGAAAGCGGTATACCGGTTCATCTGGGAAACGGTGTGCTCATATGATCATCGGCG	660
Db	7076	CAGATAGATGAAAGCGGTATACCGGTTCATCTGGGAAACGGTGTGCTCATATGATCATCGGCG	7135
OY	661	CTGCAACGCATGGGGGGGGCGTGGTCTGATATCTGACGGCCCAAGAAATTTCTGGAAACCAC	720
Db	7136	CTGCAACGCATGGGGGGGGCGTGGTCTGATATCTGACGGCCCAAGAAATTTCTGGAAACCAC	7195
OY	721	GGTCAAGGTGGCGGGGTCTCGAACGACACACGAGGCGTGTATCACGAGGACAGCCTGTGATCCG	780
Db	7196	GGTCAAGGTGGCGGGGTCTCGAACGACACACGAGGCGTGTATCACGAGGACAGCCTGTGATCCG	7255
OY	781	CGAGCCGTCGGTCAAGCGTCGCGCGGTATCTCTCAAGCGTGTGGCAATGCTATTTCCACCG	840
Db	7256	CGAGCCGTCGGTCAAGCGTCGCGCGGTATCTCTCAAGCGTGTGGCAATGCTATTTCCACCG	7315
OY	841	CAGATTCGACACCTTCGACAGACGCCGATCAAGGGGCGCGCCTCATTCGAGCCATAGCGCTGT	900
Db	7316	CAGATTCGACACCTTCGACAGACGCCGATCAAGGGGCGCGCCTCATTCGAGCCATAGCGCTGT	7375
OY	901	CGTCAAGCGGCGCGCAATGTGTCTGGGAAACGCGACCTCTGTATCCGTTCATTTGCCCGGACG	960
Db	7376	CGTCAAGCGGCGCGCAATGTGTCTGGGAAACGCGACCTCTGTATCCGTTCATTTGCCCGGACG	7435
OY	961	AATGGGCGACAGGGCGCGCGCACCTTTGGGGCGAAAGATCCGTGTCTGTGGCAGACCAAGT	1020
Db	7436	AATGGGCGACAGGGCGCGCGCACCTTTGGGGCGAAAGATCCGTGTCTGTGGCAGACCAAGT	7495
OY	1021	GTGCTGTGTCCGAGGGGGGCGGACCGCGCGGTGTGAGGATACAGATATGGCGCATCCGGTCTGCG	1080
Db	7496	GTGCTGTGTCCGAGGGGGGCGGACCGCGCGGTGTGAGGATACAGATATGGCGCATCCGGTCTGCG	7555
OY	1081	GTGCGGAACGGCAAGCGCGATCAAGCGCACTGGGACAGCCCTGGCGCTCCGCGATCAAGCAATC	1140
Db	7556	GTGCGGAACGGCAAGCGCGATCAAGCGCACTGGGACAGCCCTGGCGCTCCGCGATCAAGCAATC	7615
OY	1141	ATGGCTCAT 1149	
Db	7616	ATGGCTCAT 7624	

RESULT 6
US-10-810-733-7/c
Sequence 7, Application US/10810733
Publication NO. US20050014219A1
GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Co., Inc.
APPLICANT: Cheng, Qiong
APPLICANT: Tao, Luan
APPLICANT: Sedkova, Natalia
TITLE OF INVENTION: GENES ENCODING CAROTENOID COMPOUNDS
FILE REFERENCE: CL2385 US NA
CURRENT APPLICATION NUMBER: US/10/810,733
CURRENT FILING DATE: 2004-03-26
PRIORITY APPLICATION NUMBER: US 60/488,183

;; PRIOR FILING DATE: 2003-07-17
;; PRIOR APPLICATION NUMBER: US 60/527,083
;; PRIOR FILING DATE: 2003-12-03
;; NUMBER OF SEQ ID NOS: 22
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 7
;; LENGTH: 1164
;; TYPE: DNA
;; ORGANISM: Pantoea stewartii DC413
US-10-810-733-7

Query Match 21.7%; Score 248.8; DB 21; Length 1164;
Best Local Similarity 54.2%; Pred. No. 1.5e-53;
Matches 605; Conservative 0; Mismatches 487; Indels 24; Gaps 4;

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QY 42 GCACGGCCCTGCAGACGCGGAATGCGGCGCTCCGGGTGACGATGCGAAGCCGGTCGGCA 101
DB 1120 GCACGCCGCCCGACACCGGACCGGCGCTTGCCTTAAGAAATGCGCGCGGTGCGCA 1061
QY 102 ATGTACGCGCCCGCGCATGAAGCCGCTCGATCAGCGGCTGCGGCAAGCGGTAGAACCGCT 161
DB 1060 GCGTACGCGCGTCCGGGTAAACCGGGCGATCAGCCCTCGGGCAAGCGGTAAAGCGCT 1001
QY 162 GCACGACGCGATGCGACGCGTGGCGGCGACCGCGGAACAGCATCCGCTTCAGACGCC 221
DB 1000 GCATTACGCGCGACCGCGCATCGCCCTCGCGCGCGCAAGAACAGCATGCGGTTAAGCATGC 941
QY 222 GCAGAGAGCGGTGCGGATCGCGGCGCATGATGGGCCAGCGCGCGCACCGCGCGCGCGG 281
DB 940 GGAAGAAAGCCCTGTTTAAACGACGCTGCTGCGCAAGGCGTGAATACCGCGCGCAGCG 881
QY 282 ACGCGCTGCTCAGTGCAGCGC---GCCGCGATGCGATCCGCGACTTGCGGGATAGGGCA 338
DB 880 CCTCAGGGGAGAAGTCCGCGCTCGCGGCGAGGCGGTCCGCGACGCTGCGCGCAAGCGCA 821
QY 339 GCGAATATCCGCTGACGCGGCTGGAACAGCCCTGCGCCCGACCCAGCCGACCGCCCT 398
DB 820 GCGAGTAGCCGCTGCTGGGTGAAAAAGCCCGCGCGCGACGCGCGACG-----CAGG 770
QY 399 GCGCGCTGCTGCGCGCGAAGCCGATGGCGTCAATGGGCGCGCGCGCGATGGCGAGATGCC 458
DB 769 GCGCGCGATGATGCCAAGAGCGGTCAAAATCGCCCGCGCGCGTAAATGCGCGCGCGCC 710
QY 459 T---TTGCGCGCGCATCTCTGCGCGGTCCAGCGCCCGCTGCGCGCATAGTCCAGCGACG 515
DB 709 GCTCTTGGGCGACGACGCTCTCAGCTGCGACGCTTGGGGGTGGGTAGTGGCAGATAT 650
QY 516 CCTGCGCGACGCGCGCATGCTTCATGCGCGCGCTGCTGTAAGCGCGTATCTTGATTA 575
DB 649 TCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCTTAAATATAGTGGTATCTTCATCA 590
QY 576 GGAATGCGGCTGGGATGGAAGGCGAGCATAGATGAAGGGGTAAACCGGTCAATCTGCGAA 635
DB 589 GCGAAGCGCGTCCGCGAGCGGCGAGGTATAGCGAAGGATAGCCCTCTGCTGATTCGA 530
QY 636 CCGTCCGCTGCATGATCATCGGCGCTCGACGCGCATGGGCGGCGTGTCTGATTCGA 695
DB 529 CCGCGCGCTGCATCAAAATGCGCGCTTCCAGCTGAGCGGCGTGGCTCAGGCGCACTCT 470
QY 696 CCGCGCGAATTTCTGAAACCCACGCTGAGGTGCGGGTCTTCGACGCGACCAACGCGGCT 755
DB 469 GACCGCAAAAAGCATGAAGCCATCTGACGAGGCGCGCTGCGGCTGATAGCGCGCGCT 410
QY 756 CGATACCGACGAGCGCTGATCCGCGACCGCTTCATGCGGTGCGCGCGGTATGTCGA 815
DB 409 CAATGACGCGCGCGCGCGCGACATTCGCGCTGCGAGCTGCAAGTATGCGGGCGCG 350
QY 816 GCGTCGCGACATGCGGATTCACACCGACATCGACACCT-----GACGACGCGCGCA 866
DB 349 TCGTGGCGACGCTGTAGCGCGGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCACTCT 290
QY 867 TCAGCGCGCGCGCTGATGAGCGCATGCTGTCTGACGCGCGCGCGAATGCTCGGAA 926
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DB 289 CAAGCGCGCGGAGTGAACGAAAAATACCGCTGTAAAGTGGCGCTCAGCGCGGAA 230
QY 927 ACGGACCTCTGATCCGTCATTGCGCGCGACGATGGGCGACAGCGCGCCAGCCATT 986
DB 229 ACCGTACCTCTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 170
QY 987 CCGGCGGAAAGATCCGTGTGCTGCGCGAGACAGAGTGTCTGTTCGAGGGGCGCGACCG 1046
DB 169 CCGCGCTGATCTCTTCTGTGAAGACACAGTGTGATTCACCGCGCGCGCGCGCGCG 110
QY 1047 CCGTGAAGATACGATGCGGCGCATCCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 1106
DB 109 CATCAAGACACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 50
QY 1107 CACCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1142
DB 49 CCGTGGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14
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RESULT 7

US-10-810-733-20/c
; Sequence 20, Application US/10810733
; Publication No. US20050014219A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Co., Inc.
; APPLICANT: Cheng, Qilong
; APPLICANT: Tao, Luan
; APPLICANT: Sedkova, Natalia
; TITLE OF INVENTION: GENES ENCODING CAROTENOID COMPOUNDS
; FILE REFERENCE: CL2385 US NA
; CURRENT APPLICATION NUMBER: US/10/810,733
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 60/488,183
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 60/527,083
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 9127
; TYPE: DNA
; ORGANISM: Pantoea stewartii DC413
US-10-810-733-20

Query Match 21.7%; Score 248.8; DB 21; Length 9127;
Best Local Similarity 54.2%; Pred. No. 1.3e-53;
Matches 605; Conservative 0; Mismatches 487; Indels 24; Gaps 4;

```
QY 42 GCACGGCCCTGCAGACGCGGAATGCGGCGCTCCGGGTGACGATGCGAAGCCGGTCGGCA 101
DB 6138 GCACGCCGCCCGACACCGGGACCGGCGCTTGCCTTAAGAAATGCGCGCGGTGCGCA 6079
QY 102 ATGTACGCGCCCGCGCATGAAGCGCTGATCAGCGGCTGCGGCGAGCGGTAGAACGCT 161
DB 6078 GCGTACGCGCTCCGCGTAAGACCGGCGATAGCCCTCGGCGAGCGCGTAAGAGCGCT 6019
QY 162 GCACGACGATGCGAGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 221
DB 6018 GATTAACGCGCGACGCGCGCGATGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 5959
QY 222 GCAGAGACGCTGCGGATCCGCGCGATGATGAGCGCGCGCGCGCGCGCGCGCGCGCG 281
DB 5958 GGAAGAAAGCCCTGTTAGCGCACGCTGCTGCGCAAAAGCGGTAAATGACGCGCGCG 5899
QY 282 ACGCGCTGTCAGGTGCGCG---GCCGCGATGCGATTCGCGCACTGCGCGCGCATAGGCA 338
DB 5898 CTTCAAGGAGAGAAAGTCCGCTCTTGGCGAGCGCGCTTGGCGAGCGCTGCGCGCGCG 5839
QY 339 GCGAATATCCGCTGACGCGGCTGGAACAGCGCTGCGCGCGCGCGCGCGCGCGCGCG 398
DB 5838 GGAAGTAGCGGCTGCTGGGTGAAAAAGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 5788
QY 399 GCGCGTGTGCGCGCGCAAGAGCGTATGCGTATGCGCGCGCGCGCGCGCGCGCGCGCG 458
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Db 5787 GGAGCGGATGATGTCAGAAAGCGGTGCAAAATCGCCCGCCAGCTAATCGGAGGCGCCCG 5728
Qy 459 T---TTGCGCCGCAATCTCTGCGCGGTCCAGCCCGCCCTGGGGCAATATCCAGGAGC 515
Db 5727 GCTCTTGGCGGACAGCGTCTCCAGCTGCGCCGCTGGCGGGTGGGTGTCCAGATAT 5668
Qy 516 CTGCGCCAGCGGCGCATCTGTCAGATCGCGCGCTGCTGTAGCGGATCTCTGATCA 575
Db 5667 TCTGCGCGCGCTGCGCGCTGCGCGAGAGCGCGCTGTTAATATAGTGGATCTTCAATCA 5608
Qy 576 GGATGCGGTGGAGCTGAAGGCGAGAGATAGATGAAGCGGTACCCCTCATCTGCGGA 635
Db 5607 GCAGAGCGCGTGGCGAGAGCGGAGAGGATAGAGAGAGCATAGCCCGCTGCTGATCA 5548
Qy 636 CGGTCCGCTGATGATATCGGCGCTCCAGCGCATGGGGGGGTGGGTCTGATCTGCA 695
Db 5547 CGCGCGCGCTCATCAAAATCGGCGCTCCAGCTGATCGGCTGGCTCAAGCGCCACTCT 5488
Qy 696 CGCCCGCATTTCTGGAACCCAGCGGTGAGTGGCGGGGTCTGAGCGGACCAAGCGGCGT 755
Db 5487 GACCGCAAAAGACTGAAGCCATCTGAGGCGCGCTGCGGCTGATAGCCGCGCGCT 5428
Qy 756 CGATCAAGAGAGCGCTGATCGGAGCGCTGCTGCTGAGCGCGGTATCTGCA 815
Db 5427 CATGACGCGCGCGCGCGCGAGCACTTCCGCTGGGAGCTGCAATGATCGGCGCG 5368
Qy 816 GCGTCCGCAATGCTGATTCACCGCATGATCAACCTT-----GAGAGCGCCGA 866
Db 5367 TGTGCGCGAGCGGTCTGATTAAGCGCGAGCGCTGCGCGAGCGCTGCGCGAGCACTCT 5308
Qy 867 TCAGCGCGCGCGCTGATGAGCACTAGCGCTGCTGCAAGCGCGCGGATGCTGCGGA 926
Db 5307 CAAGCGCGCGGAAAGTACGCAAAATAGCGCTGTTAAGCTGGCGGTGACGCGCGGA 5248
Qy 927 AGCGCACTCTGATCTGATCTGATTCATTCGCGCGAGAAATGGGCGCGCGCGCATT 986
Db 5247 AGGTGCTCTGATGCTGCGCGAGCGGTGGCGCGAGCGCGCGCATGATGCTGGG 5188
Qy 987 CGGCGAAAGATCTGCTGCTGCGAGAGCAAGTGTGCTGCTGCGAGGGCGCGAGCGG 1046
Db 5187 CGCGCTGATCTCTCTGCTGAAGCACAGGTGTGATGCTGCGCGCGGTGGG 5128
Qy 1047 CGTCAAGCATCAAGATGCGCGCATCGGCTGCTGCGGAGAGCGAGCGCGATGAGG 1106
Db 5127 CATCAAGCACAGAGCGCGAGCTGCGGCTGAGCGCTTCAAGCGAGCGAGCGAGC 5068
Qy 1107 CACCGGACAGCGCGCGCGCGCGCATGAGCAT 1142
Db 5067 CGTTGCGCAGAGCGCGCGCGAGCAAGCATGATCAT 5032

RESULT 8
US-10-166-037-2/c
; Sequence 2, Application US/10166037
; Publication No. US20030087337A1
; GENERAL INFORMATION:
; APPLICANT: GIRAUD, Eric
; APPLICANT: HANNIBAL, Laure
; TITLE OF INVENTION: Isolated Carotenoid biosynthesis gene cluster involved
; TITLE OF INVENTION: in canthaxanthin production and application thereof
; FILE REFERENCE: 1721-55
; CURRENT APPLICATION NUMBER: US/10/166, 037
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 60/297, 272
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: cxy
US-10-166-037-2

Query Match 20.6%; Score 236.4; DB 14; Length 1185;
Best Local Similarity 54.0%; Pred. No. 2.1e-50;
Matches 569; Conservative 0; Mismatches 471; Indels 30; Gaps 4;

Qy 78 TCAGATGCGAAGCGGCTGCGCAATGTCAGGCGCGCGGATAGAGCGCTGATCAGG 137
Db 1102 TGAAGAGCGGAGCTTGTCTGCGGTGATGATCGGCGCGCTGAGAGCGCTGATCAGG 1043
Qy 138 GCTGCGGAGGCGGTAGAACTGCTGAGGAGGATAGGAGCGTGGCGGCGAGCGC 197
Db 1042 CCGTATGAGAGCGTAAATCTGTCAGAGATTCGGTGAAGTCCGAGGCGCTCGCGGCT 983
Qy 198 GGAACGATCTCGGTTGAGAGCGGAGCGGAGAGCGGATCGGATCGCGCATGATGAGCC 257
Db 982 TGAACGATCTCGGTTGAGAGCGGATAGTACCGCGCGGCGCAGATGTCGCGCGT 923
Qy 258 AGCGCGGAGCGCGGAGCGGCGGAGCGGCGGTGTCAGGTG-----CGCG 302
Db 922 AGCATGATGATCTGCGCGCGGTGAGCGCTGAGAGCGCGCGCTTGGCGAGCGCG 863
Qy 303 CGGATGAGCATTCGCGAGCTGCGGAGGATAGGAGCGAATATCGGTGAGCGGAGTGA 362
Db 862 CGGTAGAGAGTGGGAGAGCGGAGCGGCTCGGAGGAGAAATAGCGGTGTCGATGCA 803
Qy 363 AAGCGCTGCGCGGAGCGGAGCGGAGCGGCGGCGGCGGTGCTGCGCGAGAGCTTA 422
Db 802 CGAAGAGCGCGCGAGAGCGGAGCGGCGGCGGCTG---CGGCTTGTGAGCAGCGCG 746
Qy 423 TGGCGATAGGCGGAGCGGAGGAGGAGGAGCGGCGGCTTGGCGCGCATCTCTGCGCG 482
Db 745 AGGATGCGCGCGCGGATGAGGAGGAGGAGCGGCTGCGCGGAGATCTGAGCA 686
Qy 483 TCGAGCGCGCGCTGCGG---GATAGTCAAGGAGCGCTGCGCGAGCGCGCGCATGCTCA 539
Db 685 TCTGCGAGCGCTTGGGAGAGCGGTAGCGGCGGATGCGGTGAGGAGCACTGCTGGGGA 626
Qy 540 GATCGCGCGCTGCTGAGCGGATCTGATGAGATGCGGAGTGGAGTGAAGGGA 599
Db 625 ACTCGCGCGCGCTGCTGATGAGTGTCTCTGATCAACAGCGCGTGAAGGATGAGCGGA 566
Qy 600 GGAATAGATGAAGGAGTACCGGTCACTGCGGAGAGCGGTGCGCTCATGATCGGCG 659
Db 565 GGTGATGAGGAGGAGTACCGGTCTGCTGCGAGCGGTGCGCTCATGAGATGAGGA 506
Qy 660 GCTCAAGCGCATGAGGAGGAGTGTGATCTGATCTGAGCGCGCAAGATTTTGAAGCA 719
Db 505 CATGAGAGCGGTGCGGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCACTTGAAGCGGA 446
Qy 720 CGGTAGGTGCGGAGTCTGAGCGGAGCGGAGCGGCGTCAATCAAGAGCGAGCTGATTC 779
Db 445 GAGCGAGCGCGGAGCGGCGGCGGCGGCGGCGGATCAAGAGCGGAGCGGCGGAGG 386
Qy 780 GCGAGCGGTGCTGAGC-----GTGCGCGCGGTATCTGCGAGCGGTGCGGAGTGG 830
Db 385 TCGGCGCGCTTCAAGAGCGGAGTGTGCTGCTGCGGAGTGGCGGTGCTGCGGA 326
Qy 831 TATTCACGCGGATGAGACCTTCAAGAGCGGATGAGCGGCGCGCTGATGAGGAG 890
Db 325 GATCTCTCTCGGAAAGAGCTGCTGAGCTCGGAGCGGAGCGGCGCTGATGAGGAG 266
Qy 891 CATGAGCTGTGTCAGCGGCGGAGATGTCGGAAGAGCGGAGCTTCTGATCTGATTC 950
Db 265 GGTAGGCGGTGAGAGAGATGAGATGTCGCGGAGAGCGGAGCTTCAATTAACCGGCGAGC 206
Qy 951 CGCGCGAGAGATGAGGAGAGCGGCGGAGCGGAGCATTTGGGAGAAAGATCGGTGTGGC 1010
Db 205 GATGACGAGAGCGGTGCGAGCGGAGCGGTGCTGAGAGGATGATGAGTTCAAGGA 146
Qy 1011 AGACGAGGTGCTGCTGAGAGGCGGAGCGGCGCTGAGCATGATGCGCGCAT 1070

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Db      145 AGCTCCAGGTGATGATTCGGGCGGATCGGAGGCTTTCGATGATGACGACGGCAAT 86
Qy      1071 CCGGTCCTGGGTGCGCAAGCGGACCGGATGACGGACAGCCCGCGCGCA 1130
Db      85 CCGGCGGTGCGGTGCGGAGCCCGGACGATGACGAGCCGGCAGAGCCCGCGGATG 26
Qy      1131 TCAGCAGATC 1140
Db      25 CGATGACGTC 16

RESULT 9
US-10-808-807-5/c
; Sequence 5, Application US/10808807
; Publication No. US20040253663A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Co., Inc.
; APPLICANT: Cheng, Qiong
; APPLICANT: Tao, Luan
; APPLICANT: Sedkova, Natalia
; TITLE OF INVENTION: GENES ENCODING CAROTENOID COMPOUNDS
; FILE REFERENCE: CL2365 US NA
; CURRENT APPLICATION NUMBER: US/10/808,807
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/477,874
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/527,083
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Pantoea agglomerans strain DC404
US-10-808-807-5

Query Match      19.9%; Score 228.6; DB 20; Length 1170;
Best Local Similarity 52.8%; Pred. No. 2e-48;
Matches 595; Conservative 0; Mismatches 514; Indels 18; Gaps 4;

Qy      29 TCGGGGAGGACGCGCAGCGGCTGCGACAGCGGAATGGGGCGGCGTCCGGTGAACATGCA 88
Db      1136 TGGAGAGGAGCTTTTGTATCCCGCCGACAAATCGGACCGCGTTTGGCAAGCAGAGCGCG 1077
Qy      89 AGCCGGTCGCGCAATGTCAGCGCGCCCGGATAGAAAGCGCTCGATGAGCGGCTGCGGCAAG 148
Db      1076 GGGCGGTGCGCGAGGAGGAGTGGCGCGATATAAAAGCGGCGATGAGTGTCTGTCAAGC 1017
Qy      149 CGGTAGAACCGGTGCGACAGCGGATAGCAAGCGTGGCGGCGAGCGCGGAAACAGCATC 208
Db      1016 TGGTAAACCGGTGCGATCAAGCGCGCAGCGCTGGTGGTGTGCGCGCCAGGAAAGCATG 957
Qy      209 CGGTCAGAGCGCGGAGGAGGCGTGGCGATCCGCGCGATCGATGGGCCAGCGCGGCAAC 268
Db      956 CGGTAAAGAGCGGAGGAGGAGGCGTGTGTCGCAATGGCGCGCGGAAATCGGCGATC 897
Qy      269 GCGCGAGCGGCGGACCGGCTCGTCAGAGTGGCGGC---CGCATGGCATCCGCGACCTTC 325
Db      896 AGCTGATAGAGCGCGCGCTGATGCAATCCCGGCGCTTGGCAATGGGTTCCGCGACCGA 837
Qy      326 GCGGCGATAGGCGGACGCAATATCCGATGACGAGGAGTGAACAGCCCTGCGCCCGCCAGCC 385
Db      836 ACCGCGAGCGGCGGACGCAATAGCGGAGTGGGATGGAACAGACCGGCGCGGCGGCTG 777
Qy      386 GGCACCGCGCCCTGCGCGGTGTCGCGCGAGAGGCTTATGGCGTCATGGGCGCAGCGGATG 445
Db      776 ---ACGCGTGAATGATGAATGAGTGTGTCAGAAAGCGGCGGATCGCGGACAGGAGTATC 720
Qy      446 GGCAGGATGCGCCCTTTCGCGCGCATCTCTGGCC---GGTCAAGCGCGCGCTGGGCGGCA 502
Db      719 GGGAGGCGCCCTCTGTCTCAAGGACACCGCGGCAAGTGTGCGACCGCTCTGCGGCGGCG 660
Qy      503 TAGTCAGGAGCGCTGCGCGAGCGCGCATGCTCCAGATCGCGCGCTGTGATGCGCG 562
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Db      659 TAATCGGCAATCCGCGCGCGGCTGAATCGGCGTGAACCGTCCGAGCGCTCAATGATGTC 600
Qy      553 GTATCTTCGATCAGGATGCGGATGGAATTAAGGAGCAGATAGATAGTAAGCGGATCCCG 622
Db      599 GTGTCTTGAATAGAGGAGTGTGCGCGTGAAGCGGCGAGGATATAGACAAACCGTAGCG 540
Qy      623 TCCATTCGCGGAACGGTGCCTGATGATGATCGGCGCTGACGCCATGGGAGGCGCTGC 682
Db      539 TTGCGCTGGGCGAGCGCGGCGATTCATGAGATCGGCGCGTTAAACCGTGGGCGCGGTC 480
Qy      683 GTCTGATCTGACGCGCCACGAAATTTGTGGAACCCAGGTCAGATGGGCGGTCTCCAGC 742
Db      479 AGTTCCCACTCTTCGCGCATGAGACCGCTGATAGCCAAATGCTAGAGGTGCGGAGGCTGA 420
Qy      743 GCACCAAGGCGGTGATGACGAGGACGAGCTGATCCGCGAGCGGCTCCGTCAGCGTCGCG 802
Db      419 TAGCGCGGCGCATCATATACCGCCCGCGGTAAAGCGTCTCGTCCGTAGAGGTTACT 360
Qy      803 CCGGTATGTCGACGGTGCAGCATGCGTATTCACCGCGAGATGACACCTCGACGAGC 862
Db      359 TCTTCGCGCGCTCACCGGTGACCGGTGACGTTTGTGACGAAATTCCTTTTCATGAGCCG 300
Qy      863 CCGATCAGCGCGC-----CGCTCATCGAGCATAGGCTGTGTCAGCGCGGCG 913
Db      239 CGCATCGCTTGGGCAAAACGGGTGAGGTGATGTCAGGTAGCGGTCAATGACGAGGTGCGC 240
Qy      914 GAATGTCGGGAAACGCACTCTGATCCGTTCATTCGCGCGGACGAGATGGGCGGACAGG 973
Db      239 GACAGTTTCGAAATGAGCATCTGTACCCGTCCAGCGATGGGCGACAGGCGCGCGC 180
Qy      974 CGCGCAGCATTCGGGAGGAAAGATCCGTGTGTGGAGAGACAGAGTGTGTCGAG 1033
Db      179 CAGCGGTCTGGGCTGGCGGTATTCGTTGTGTAAGAGACAGGTGTGTTCCGCGG 120
Qy      1034 GGGCGGAGCGCGGCTGCAAGATCAAGATGGCGGATCCGCTTTCGCGGAGCGCA 1093
Db      119 GCGCGGTGCGCGCATCTCAGCATTAATACAGCAAGCGGTGATGACGCTGTGATGTCG 60
Qy      1094 AGCGGATCAGGCGCAGGACGCGCGCGCGCGCGGATCAGACATC 1140
Db      59 CAGCGATTAAGCCGTTGGCGAGCGCGCGCGCGGACGAGATCAATC 13

RESULT 10
US-10-997-844-6/c
; Sequence 6, Application US/10997844
; Publication No. US20050124033A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Pamela J
; APPLICANT: Bosak, Melissa
; APPLICANT: Tao, Luan
; APPLICANT: Sedkova, Natalia
; APPLICANT: Cheng, Qiong L
; TITLE OF INVENTION: Optimized Bacterial Host Strains of Methylomonas sp. 16A
; FILE REFERENCE: CL-2230 US NA
; CURRENT APPLICATION NUMBER: US/10/997,844
; PRIOR FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/527,083
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/527,877
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 5632
; TYPE: DNA
; ORGANISM: Pantoea agglomerans
US-10-997-844-6

Query Match      19.9%; Score 228.6; DB 22; Length 5632;
Best Local Similarity 52.8%; Pred. No. 1.7e-48;
Matches 595; Conservative 0; Mismatches 514; Indels 18; Gaps 4;
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OY	29	TCGGGACGACGCGACCGGCTTGCGACACAGCGGAATGGGCGGGCGGTCCGGTACACATGTCGA	88
Db	2014	TGAAACAGGGCTTTGATCGCCCCCAATCGGACACCGGCGGTTTGGCCAAAGACAGCGGCG	1955
OY	89	AGCCGGTGGCCCAATGTACAGGCGCCCGGCATAGAAGCCCTGATCAGCGGTGCGGACAG	148
Db	1954	GCGCGGTGCGGCGAGCGAAGCTGGCGCGGCATTAATAACGGGCGATACGTCTCTGTCAGC	1895
OY	149	CGGTAAACCGCTGACAGAGCGGATAGCGACGGTGGGCGGGCAGCCCGCGAACAGCATC	208
Db	1894	TGGTAAACCGCTGATCAGCGGCCAGCGCTGGTGGGGTGTGCGGGCCAGGAAAAAGCATG	1835
OY	209	CGGTTACAGACCGCGAGAAAGCGGTTCGGGATCCGGCGATGATAGGCCACCGCGCAC	268
Db	1834	CGGTTAACACAGCGCGAATAAGCGTTGTGTCTTCGCAATGGCGCGCGCCAAATCGCGATC	1775
OY	269	GCGGACGGGGGAGACGGGCTGTGTCAGGTTCGGGCGC---CGGATGGCATCCGCGACCTCG	325
Db	1774	AGCTGATAGAGCGCCCTGATGCTGTCGCCGCGGCTTGGGAATACGGTCCGACCGCA	1715
OY	326	GCGGATAGGGACGGAATATCCGTTGACGGGGTGGAAACAGCCCTTGCCCGCCAGCCCAAC	385
Db	1714	AACCGACAGCGGACGGAATAGCGGTGTGGGATGGAACACAGCGCGCGACGGCGCTGT	1655
OY	386	GGCACCGGCCCCCTGGCGGTGTGCGCGCAAGACCTATGGCGTCAATGGCCAGCGCATG	445
Db	1654	---ACCGCTATGATGAGAACTGGGTCCAGAAAGCGCGCGGATCGCGACAGGGTGTATC	1598
OY	446	GGCAGGATGCCCTTTGCGCGCGCATCTCTGGCC---GTTCCAGCCCGCGCTGGCGGCA	502
Db	1597	GGCAGCGCCCCCTGTTCTCTCAGCGCACAGCGCGCGAGCTCCAGCCCTGTCTGGCGGGCG	1538
OY	503	TAGTTCAGACGACGCTTGCGCCAGCGCGCATCTGTCAGATCGCGCGCTGCTGTAGCGC	562
Db	1537	TAATGGGCAATCCGCGCGGGCTGTAAATCGGCGTGAAGCGTTCGGGCGCTCAATGTATGTC	1478
OY	563	GTATCTTCGATCAGAGATGGGGGTGGGACTGAAGGGCAGACAGATAGATAGACGGTACCG	622
Db	1477	GTGTCTTCGATTAAGCAGGGTGTGCGCGCTGAGCGGCAAGGTATAGACAAACGGTAAACG	1418
OY	623	TCCATCTGCGGAACGGTGGCGGTCCATATCATTCGGGCGCTGAGCGCATGGGGGGCGTGC	682
Db	1417	TTGCGCTTGCGGACCGCGGGCATTCATCAGGATTCGGGCGCGTTAACCCCTGGGGCGCGGTC	1358
OY	683	GTCTCGATCTGACGCGCCACGAATTTTCGAAACCCACAGGTCAAGTGGGGGGGTCTCGACG	742
Db	1357	AGTTGCCATCTCTGGCGGATGAACCGCTGATAGCCAAATGTCTGAAGTGGGGAGAGGCTGA	1298
OY	743	GCACCAACGGGGGTGATCAGCAGGACGACCTCGATCCCGACGCGTCCGTCAAGCGTGC	802
Db	1297	TAGCGCGGCGCATCAATCACCGCGCCCGCGGTAAGCGTCCGTGGCTTAAGGGTTACT	1238
OY	803	CCGGTATGTCAGCGCTGCGACATGCGTATTTCCACGCGAGATGACACCTTGACGACG	862
Db	1237	TCTGCGCGCTCACCCGTAACGCGTCAAGTTTGTGACAAATCTCTTTCATCAGCGCG	1178
OY	863	CCGATTCAGCGGCG---CGCTTCGATCCAGCCATGAGCTGTCTGTCAGCGCGCGC	913
Db	1177	CGCATCGCTTGGGCAAAACGGGTGAGGGTATGTGTCAGTGAAGCCGTCAATGAGGGTGGC	1118
OY	914	GAATGATGGGAAAAACGCACTCTCGATCTCCGTCAATTTGGCGGACAGAAATGGGCGACAG	973
Db	1117	GACAGTTTCGAAAGTGAAGTGTGTAACCGCTTCACAGCAATGGGCAACCAAGGGGCGCAGC	1058
OY	974	GCGCCAGCCATTTCGGGCGAAAGATCCGTTGTGTGGCAGAACAGAGTGTGCTGTCCGAG	1033
Db	1057	CAGGCGTCTGGGCTGGCGGTGATATCGTTGTGTAAGGACACAGGTGTGTTTCCGCG	998
OY	1034	GGGCGCGACCGCGCTGACAGATCAACATGGCGCGATCCGGTCTCGGTCGCAACGGCA	1093
Db	997	GGCGGTGCGCGCATTCAGCATTTAATACAGCAAGCGTGGATGACGCTGTGTTTATGTCG	938

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Dy      1094 AGCGGATTCAGCGCAGCGCAGCGCCGCGCGGATTCAGCATC 1140
Db      937 CAGCGATTAAGCCCGTTGGCCAGCCCGCGCGACAGATCAGATC 891

RESULT 11
; US-10-808-807-18/c
; Sequence 18, Application US/10808807
; Publication No. US20040253663A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Co., Inc.
; APPLICANT: Cheng, Qiong
; APPLICANT: Tao, Luan
; APPLICANT: Sedkova, Natalia
; TITLE OF INVENTION: GENES ENCODING CAROTENOID COMPOUNDS
; FILE REFERENCE: CL2365 US NA
; CURRENT APPLICATION NUMBER: US/10/808, 807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/477,874
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 60/527,083
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 18
; LENGTH: 8814
; TYPE: DNA
; ORGANISM: Pantoea agglomerans strain DC404
; US-10-808-807-18

```

Query Match	19.9%	Score 228.6;	DB 20;	Length 8814;
Best Local Similarity	52.8%	Pred. No. 1.7e-48;		
Matches 595; Conservative	0;	Mismatches 514;	Indels 18;	Gaps 4;

OY	29	TCGGGCAAGGCAAGCCCAACGGCTGTGGACAAGCGGAAATGGGGGCGGCGTCCGGTATGACATGTGGA	88
Db	5559	TGAGACAGGGGCTTTGATTCGCCCCGACAAATCGGCACCGCGCGTGTTCACAGACGACGAGCGC	5500
OY	89	AGCGCGTCCGCAATGTCACGGCGCGCCGGGCAATAGAAAGCGCTGATCAGACGGCTGCGGAGG	148
Db	5499	GCGGCGTTCGGCGGAGCGAAGTGGCCGGGCAATAAACCGGGGGAATCACTGTCTCCTCAAGC	5440
OY	149	CGGTAGAACCGCTTCAGACAGGCGATGACGACGCTCGGGCGGAGCGCCGGAAACAGCATC	208
Db	5439	TGTAAACACGCTGCATCACCGCCAGCGCTGGTCGGGTGTCGCGGCACGGAAACATG	5380
OY	209	CGGTTTCAGCAGACCGCCAGAAAGCGGTCCGCAATCCGCGGATGATGATGCGCCAGCCGCGCAC	268
Db	5379	CGGTTAAGCAGGCGCGGAAAAAGCGTTGTGTCTGCGCAGTGGCGCGCCGGGAAATTCGGCAATC	5320
OY	269	GCGGACGCGGCGGACGCGGTCGTAAAGTCCGCGCGC---CGGATGGGATCCGCGACCTGC	325
Db	5319	AGCTGATAGAGCGCGCCCTGTATGCAATCCGACCGCGTTGGCAATCGGTCGCCACGCGGA	5260
OY	326	GCGCATATGGGCGACGCAATATCCGGTACGCGGGTGGAAACAGCCCTGCCCCAGCCCAAC	385
Db	5259	ACCGCCAGCGGCAACGAATAGCGGTGTGGCAATGGAACAGACCGGGCGGACGCGCTG	5200
OY	386	GGCACCGCCCCCTGCGCGTGGTCCGCGCCAGAAAGCTTATGGCGTATAGGCGCAGCGCATG	445
Db	5199	---ACCGCTGATGATGAACCTGGTTCAGAAAGCGCGCGGATGCGCGGACAGGGTATTC	5143
OY	446	GGCAGGATGGCCCCCTTTCGCGCGCGATCTCCMGGCC---GGTCAAGCCCGCGCTGGCGGCA	502
Db	5142	GGGAGCGCCCCCTGTCTCTCAACGACACAGCCGCGCAAGCTGCGACGCCCTGTGCGGGCG	5083
OY	503	TAGTCCAGCGACGCGCTCGCCAGCGCCCAATGTCACGATCCGCGCGCGTGCCTAGACGC	562
Db	5082	TAAATGGCAATCCGCGCGCGCGGTGAATTCGGCGGTGAGCGGTCCGCGGTCAATGTATGTC	5023
OY	563	GTAATCTCGATCAGGAATCGCGGTGGGACTGAAGGGCGACGATGATGAAGCGGTACCCG	622
Db	5022	GTCGCTTCGTATTAACAGAGGTGTCCGCGCTTAGCGCGCGAGGTATTAACAAGCGGTACCG	4963

Qy	623	TTCCATCTGCGGAAGGCTGCGGTCCATGATATATCGGGGCGTTCGACGCAATGGGGGGCGTCG	682
Db	4362	TTGCCCTGGGGGAGCGGGGCATTCATCAGGATCGGGGCGCTTAAACCGGTGGGGGCGCGTC	4903
Qy	683	GTCTCGATCTCTGACGCGCCACGAATTTTCTGAAACCCACAGGTCAAGTGCGGGGGTCTCGAC	742
Db	4302	AGTTGCCACTCTCTGGCCGATATAAGCCTTGATAGCCAAATCTGAGAGTCCGGGAGGGCTGA	4843
Qy	743	GCACCAACGGGGGCTGATACGCGACAGCGACCTCGATCCGCGAGCCGTCGTCAGCGTCGCG	802
Db	4842	TAGCCGCGGGCCATCAATCATACGCGCCCGGCGGTAAAGGTCGTGTCGTGCTGAGGGTTACT	4783
Qy	803	CCGGTATCTCTCAAGCTGTCGCAATGCGTATTTCCACCGCGAATGCAACACCTCTGAGCAAC	862
Db	4782	TCTCTGCCGCTCACCCCTGACACGATCAAGTTTCTCAGCAAAATTTCTTTTCATCAACCGC	4723
Qy	863	CCGATTCAGCGCGGC-----GGCCTCGATTCAGGACATGACCTGTCGTGACGGCGCGC	913
Db	4722	CGCATCTGTTGGGCAAAACGCGTGAGGTGATNGTCAAGTAGCCGTCAATGCAAGGTGGC	4663
Qy	914	GAATGTCGCGAAACGCGCACTCTCTGATCCGTCATTTCGCGCAGCAATGGGCGAGAG	973
Db	4662	GACAGTTCGGAAGTGAAGCTGTAACCCGTCCAGAGCATGGGCCACCAAGGGGGCGCACG	4603
Qy	974	CGCGCAAGCCATTCCGGCGGAAAGATCCGCTGTCGTGGCAGACCAAGTGTGCTGTGTCGAG	1033
Db	4602	CAGGGGTGCTGGGCTGGGGTGATATCGHTTGGTGAAGGACACAGATGTGGTTTCCGCG	4543
Qy	1034	GGGCGCGACCGCGGCTGAGCATCAGATGCGCGCATTCGGTCTGCGGTGCGGAAACGGCA	1093
Db	4542	GGCGGTGTCGCGCACTCCAGCATTAATTCAGCAAGCGTCGATGACGCTGTCTTAACTGCG	4483
Qy	1094	AGCGGATCAGGGCACCGGACAGCCCGCGCCGCGATCAGCAGATC 1140	
Db	4482	CAGGGAATAAAGCCGTTGGCCAGGCCCGCGCGACAGATCAAGATC 4436	

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RESULT 12
US-10-997-844-41/c
; Sequence 41, Application US/1097844
; Publication No. US20050124033a1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Pamela L
; APPLICANT: Bosak, Melissa
; APPLICANT: Tao, Luan
; APPLICANT: Sedkova, Natalia
; APPLICANT: Cheng, Qiong L
; TITLE OF INVENTION: Optimized Bacterial Host Strains of Methylomonas sp. 16A
; FILE REFERENCE: CL-2230 US NA
; CURRENT APPLICATION NUMBER: US/10/997,844
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: US 60/527,083
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/527,877
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 8814
; TYPE: DNA
; ORGANISM: Pantoea agglomerans
US-10-997-844-41

```

Query Match Similarity: 52.9%; Score 228.6; DB 22; Length 8814;
 Best Local Similarity: 19.8%; Pred. No. 1,7e+48;
 Matches 595; Conservative 0; Mismatches 514; Indels 18; Gaps 4;

QY 29 TCGGCGACGACGCGACCGCCTTCGCACACGGGATGGCGCGCGCGCTCGCGTACCATGCGGA 88
 Db 5559 TGGAGCAAGGCGCTTGTATGCGCCCGACATCGGCACCGCGGCGTTGGCCAGACGACGGCGGC 55000

QY 89 AGCCGCTGGCGCCATGTACAGGCGCCCGGCATAGAAAGCGCTCGATCAGCGCGCTCGCGGCAG 148

Db	5499	GC	CGCGGTTCGCGGAGCCGAGCTGGCCGGCATTAATAACGGCGGATCAGTGTCTCTCAAGC	544.0
Oy	149	CG	GTAGAACCGCTTCACGACGGCGATATAGCAGCGTTCGCGCGGCGACGCGGACACGATC	208
Db	5439	TG	GTAAACCGCTGCATCAACGCGCCAGCGCTGGTCGGGGTGTGCCGCGAGAAAGCATG	538.0
Oy	209	CG	GTTCACGACCGCAGGAAGGGTTCGGATTCGCGCGGATTCGATAGGCCACGCGGCAC	268
Db	5379	CG	GTAAAGCAGCGCGGAAAGCGTTGTGTCTCGACAGTGGCGCGCGGCAATTCGGCATC	532.0
Oy	269	GC	CGACCGGCGGAGACGCGGTGTCGATGAGGTCCGCGC---CGGATATGATCCCGCATCTG	325
Db	5319	AG	CTGATATGAGCGCGGCTTATGATATCCGCGCGGTGGGAAATGGGTTCGCGACGGCA	526.0
Oy	326	GC	GGCATATGGGCGACGGAATATCCGATGACGGGGTGGAAACAGCCTTCCCAAGCCCAAC	385
Db	5259	AC	CCCGACGGCGACGAAATACCGGTGGTGGCATATGAAACAGACCGGCGCGACGGCGCTG	520.0
Oy	386	GG	CACCGCGCCCTTCGCGGTGTCGCGGCAAGCTATATGGGTGATATGGGCGCAGGCGATG	445
Db	5199	---	ACCGGCTGATATATGAACTGTATCGGAAAGCGCGCGGATGCGCGGACAGGGTATTC	514.0
Oy	446	GG	CAGAGATATGCCCTTTCGCGCGCGGATCTCTGCGC---GGTCCAGCGCGCGCTGGCGGCA	502
Db	5142	GG	CAGCGCGCCCTTCTTCTTCTACGACACAGCGCGCGCAGCTGCGACGCTGCGTGGCGG	508.0
Oy	503	TAT	GTCCAGCGACGCGCTGGCGCCAGCGCGCATGTTCCAGATGCGCGCGTGCCTGTATGCGC	562
Db	5082	TA	ATCGGCAATCCGCGCGCGGCTGAAATCGCGCTCGAGCTCGGCGCGTCAATGATGTC	502.0
Oy	563	GT	ATCCCTGATCAGAGATGCGGGTGGAGCTGAAAGGCGGACAAATATGATATGAACGGATACC	622
Db	5022	GT	GTCTTCGATTAACAGAGGTATCGCGCTGAGCGCGGATATATGAACAAGGGATAGCGC	496.0
Oy	623	TC	CATCTGCGGAAAGGTGCGCTCCATGATTCATCGGCGCGCTCGAGCGCATGGGCGGCGTGC	682
Db	4962	TT	GGCCCTGGGAGACGCGCGGCATTCATCAGATTCGGGCGCGTAAACCGTGGGGCGCGGT	490.0
Oy	683	GT	CTCGATCTCGAGGCCCAAGATTTCTGGAAACCCACGATCGTAGGTGCGGGTCTTCAGC	742
Db	4902	AG	TGGCCACTCTGGCGCATGAACGCGCTGATAGCAATGCTGAGGTGGGCGAGGGCTGA	484.0
Oy	743	GC	ACACGCGGGGTGATATTCACGACGAGCGCTGATCCGCGGACGCGTCCGTACGCGTCCG	802
Db	4842	TAG	CGCGGCATCATATACCGCGCCCGGCTAAAGCTCGTCCGTCTGAGGGTTACT	478.0
Oy	803	CC	GGATATGTCACAGGTCGCGACATATGCTATTTCCACCGCAGATCGACACCTTCGACGAC	862
Db	4782	TC	CTGCGCGGCTCACCCGAGACAGGTTCACGTTTGTACCAAAATTCCTTTATCAGCCCG	472.0
Oy	863	CC	GATCAGCGCGC-----CGCTCGATTCGAGCCATATGCTGTCTCAGCGCGCGC	913
Db	4722	CG	ATCGCTTGGGCAAAACGCGGTGAGGTATGTGTCAGGTAGCCGTCAATGACGGGTGCGC	466.0
Oy	914	GA	ATATGTCGGGAAACGCGACCTCCGATCCGTCATTTGCGCGGACGAAATGGGCGACAGG	973
Db	4662	GA	CACTTCGGAAGTGAACGTTCGATCCCGTCCAGCGATGGGCCACACGAGGCGCCAGC	460.0
Oy	974	CG	CGCGCAGCATTTCCGCGGGAAGATCCGTGTCGTGGCAGGACAGAGTGTCTGTATCCGAG	103.0
Db	4602	CAG	CGTGTCTGGGCTGGCGGTGATATCGATTTGGTAAAGGACAGAGTGTGGTTTCGCGG	454.0
Oy	1034	GG	CGCGCAGCGCGCGGTGAGCATCATCAGATGCGCGCATCCGTTCTGCGGTTCGGAACGGCA	109.0
Db	4542	GG	CGCGGTGCGCGCACTCCAGCATTAATACAGCAAGCTCGGATGACGCTGCTTTAGTCGC	448.0
Oy	1094	AG	CGGATCAAGCACCGGACAGCCCGGCGCGCGGATCAGACAGATC	114.0
Db	4482	CAG	CGATTAAGCGCGTTGGCCAGCGCCCGCGCGACAAATAGATC	443.0

RESULT 13


```
QY 278 GCGAGCGGCTGTCAGTCCGCGC-CGCGATGCGATCCGCACTCCGCGCATAGGG 336
DB CGTGTAGAGCTCGCGGCGAGCGTGTGCAATCTTCTCCGCGAGCGCACCGCGCGGG 829
QY 337 CAGCGAATATCCGGTGAACGGGGTGAACAGCCCTTCCGCGCGCAACCGGACCGCCC 396
DB 828 CAGCGAGTAACCGGTGTGGCGTGAACAGTCCGCGCGCGACCGCGTGCAGAGTTGGCC 769
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DB 768 GTGCTGTCTTGTGCGAAGATGATGATATCGCGCTGAGCGGTGATCGGAGGAGCCGG 709
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DB 708 CTCTCTCGCGCAGCTGCGCGCAAAATTCAGCGCGCGCTGTGGGCAATATCCGTATGTC 649
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DB 588 TAAAGCGCTGCGCATGAGCGGCGAGGCTGAACAAAGCGATACCTGTGCTGATGAC 529
QY 637 GGTGCGCTCATGATCATGATCGAGCGCTCGAGCGCTATGAGGGGCGTGTGATCTGAC 696
DB 528 GCTGCGCTCATCATATGATGATGCTGTGCGAGCGCATGCGCGCGCGCATGTCACCTCG 469
QY 697 GCGCGAATTTCTGGAACCGACGCTGAGGTGCGGGGTCTGACGCGGACCGACGCGCTTC 756
DB 468 ACCGCAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 409
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RESULT 15
US-10-804-677-18/c
; Sequence 18, Application US/10804677
; Publication No. US20040224383A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Cheng, Qiong
; APPLICANT: Tao, Luan
; APPLICANT: Sedkova, Natalia
; TITLE OF INVENTION: GENES ENCODING CAROTENOID COMPOUNDS
; FILE REFERENCE: CL2346 US NA
; CURRENT APPLICATION NUMBER: US/10/804,677
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/ CURRENT FILING DATE: 2004-03-19
/ PRIOR APPLICATION NUMBER: US 60/468,596
/ PRIOR FILING DATE: 2003-05-07
/ PRIOR APPLICATION NUMBER: US 60/527,083
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 18
/ LENGTH: 8675
/ TYPE: DNA
/ ORGANISM: Pectobacterium cyrripedii DC416
US-10-804-677-18

Query Match 18.5%; Score 213; DB 20; Length 8675;
Best Local Similarity 51.4%; Pred. No. 1.5e-44;
Matches 573; Conservative 0; Mismatches 530; Indels 12; Gaps 3;

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Job time : 832.57 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 19:57:05 ; Search time 309.581 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	1149	100.0	1149	3	US-09-298-718-8
C 3	1149	100.0	1149	3	US-09-546-969-8
C 4	1149	100.0	1149	3	US-09-547-267-8
5	1149	100.0	8625	3	US-08-980-832-1
6	1149	100.0	8625	4	US-09-920-923B-1
7	1149	100.0	11233	3	US-08-980-832-27
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C 9	640.8	55.8	1161	1	US-08-663-310-5
C 10	640.8	55.8	1161	2	US-09-006-491-5
C 11	640.8	55.8	1161	3	US-09-335-919-5
C 12	640.8	55.8	2886	1	US-08-663-310-7
C 13	640.8	55.8	2886	2	US-09-006-491-7
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C 19	174.8	15.2	1149	1	US-07-783-705A-9
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C 24	59.2	5.2	1998	3	US-09-382-106-1
C 25	59.2	5.2	2229	4	US-09-252-991A-3240
C 26	59.2	5.2	2709	4	US-09-252-991A-3326
C 27	56.2	4.9	1254	4	US-09-252-991A-11478

C 28	56.2	4.9	1524	4	US-09-252-991A-11455	Sequence 11455, A
29	56.2	4.9	2028	4	US-09-252-991A-11416	Sequence 11416, A
30	55.8	4.9	1125	4	US-09-252-991A-6994	Sequence 6994, Ap
31	55.8	4.9	1929	4	US-09-252-991A-7017	Sequence 7017, Ap
C 32	55.8	4.9	1947	4	US-09-252-991A-7111	Sequence 7111, Ap
C 33	54.4	4.7	2364	4	US-09-902-540-6412	Sequence 6412, Ap
C 34	54.4	4.7	2461	4	US-09-902-540-6412	Sequence 434, Ap
C 35	53.8	4.7	4257	2	US-08-690-473-1	Sequence 1, Appl
C 36	53.8	4.7	4257	3	US-08-843-659-1	Sequence 1, Appl
C 37	53.8	4.7	4257	3	US-08-843-659-1	Sequence 1, Appl
C 38	53.8	4.7	4257	4	US-09-825-288A-1	Sequence 1, Appl
C 39	53.8	4.7	12001	1	US-08-458-568A-11	Sequence 11, Appl
C 40	52.8	4.6	12173	4	US-09-902-540-1022	Sequence 1022, Ap
C 41	52.4	4.6	741	4	US-09-724-797-73	Sequence 73, Appl
C 42	52.4	4.6	3783	4	US-09-902-540-4846	Sequence 4846, Ap
C 43	52.4	4.6	21758	4	US-09-902-540-1238	Sequence 1238, Ap
C 44	52	4.5	4826	3	US-09-192-983-3	Sequence 3, Appl
C 45	51.8	4.5	1294	4	US-10-151-832-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-660-645A-8/c
Sequence 8, Application US/08660645A

Patent No. 6087152
GENERAL INFORMATION:

APPLICANT: Hohmann, Hans-Peter

APPLICANT: Pasamontes, Luis

APPLICANT: Tessier, Michel

APPLICANT: Van Loon, Adolphus

TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSER: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street

CITY: Nutley

STATE: NJ

COUNTRY: USA

ZIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,645A

FILING DATE: 07-JUN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95108888.9

FILING DATE: 09-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Pokras, Bruce A.

REGISTRATION NUMBER: 32,748

REFERENCE/DOCKET NUMBER: RAN 6002/170

TELECOMMUNICATION INFORMATION:

TELEPHONE: (201) 235-5801

TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1149 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-660-645A-8

Query Match

Best Local Similarity 100.0%; Score 1149; DB 3; Length 1149;

Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1089 AATGGGCGGCGGCGTCCGCTGACATGCGAAGCCGCTGCGCAATGTCAGAGCGCCCGGCATA 1030
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QY 181 GTCGGGCGGCGGACCGCGGAAACGATCCGCTTACAGACCGCGAGAACCGCTCGCATC 240
DB 969 GTCGGGCGGCGGACCGCGGAAACGATCCGCTTACAGACCGCGAGAACCGCTCGCATC 910
QY 241 CGCGCGATCGATGAGCGGCGGACCGCGGACCGCGGACCGCGGACCGCGGACCGCGGACCG 300
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DB 849 CGCGCGATCGATGAGCGGCGGACCGCGGACCGCGGACCGCGGACCGCGGACCGCGGACCG 790
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QY 481 GGTCCAGCGCGCGCTGCGGACCGCGGACCGCGGACCGCGGACCGCGGACCGCGGACCG 540
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DB 609 ATCGCGCGCGTCTGAGCGGCGGATCTCGATCAGAGATCGGCGGAGAGCTGAGAGGCGAG 550
QY 601 CAGATGATGAGAGCGGATCTCGGCTGATCTGCGGAAAGCGTCCGCTCATATCATTCGAGG 660
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DB 369 CGAGCGCTCGCTGAGGCTGCGGCGGCTGCTCGACCGCTGCGGAACTGGGTATTCACCG 310
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QY 1021 GTGCTGCTCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
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QY 1141 ATGGCTCAT 1149
DB 9 ATGGCTCAT 1
RESULT 2
US-09-298-718-8/c
; Sequence 8, Application US/09298718
; Patent No. 6124113
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Pasamontes, Luis
; APPLICANT: Tesler, Michel
; APPLICANT: van Loon, Adolphus
; TITLE OF INVENTION: FERMENTATIVE CANOTENOID PRODUCTION
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingstland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,718
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/660,645
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pokras, Bruce A.
; REGISTRATION NUMBER: 32,748
; REFERENCE/DOCKET NUMBER: RAN 6002/170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-5801
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1149 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-298-718-8
Query Match 100.0%; Score 1149; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.1e-225;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1149 TCATGCTCTCTCTCTGAGCAGAGGAGCGTTGAGGACAGCAGCGACCGCTCGCAGACGCG 1090
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DB 1089 AATGGGCGGCGGCGTCCGCTGACATGCGAAGCCGCTGCGCAATGTCAGAGCGCCCGGCATA 1030
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QY 181 GTCGGGCGGCGGACCGCGGAAACGATCCGCTTACAGACCGCGAGAACCGCTCGCATC 240
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Db	609	ATCGCGCGCGTTCGTGTAGCGCGTATCTTCGATTCAGGATGCGGGTGGGACTGAAAGGCGAG	550
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OY	901	CGTCAGCGCGCGCGAATGATGCTGGGAAACGCGACCTTCGATCCGTCATTCGCGCGCGAG	960
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OY	961	AATGGGGCGACAGCGCGCGCGACATTCGGGGCGAAGATTCGTTGTGTGGCAGAGACCAAGT	1022
Db	189	AATGGGGCGACAGCGCGCGCGACATTCGGGGCGAAGATTCGTTGTGTGGCAGAGACCAAGT	130
OY	1021	GTCGTGTGTCAGAGGGGCGGACCGCGCGTTCGAGCATCAGATGCGCGCATCCGATCTGCG	1088
Db	129	GTCGTGTGTCAGAGGGGCGGACCGCGCGTTCGAGCATCAGATGCGCGCATCCGATCTGCG	70
OY	1081	GTCGCGAACGCGCAACGCGGATACGGGCACCCGGAACAGCCCGCGCCCGCGATCAGCAATC	1144
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RESULT3
US-09-546-969-8/c
; Sequence 8, Application US/09546965
; Patent No. 6207409
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Paasmontes, Luis

```

1  APPLICANT: Tessier, Michel
2  APPLICANT: van Loon, Adolphus
3  TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
4  NUMBER OF SEQUENCES: 47
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Hoffmann-La Roche Inc.
7  STREET: 340 Kingdland Street
8  CITY: Nutley
9  STATE: NJ
10 COUNTRY: USA
11 ZIP: 07110
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent'n Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/09/546,969
19 FILING DATE:
20 CLASSIFICATION:
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/660,645
23 FILING DATE:
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Pokras, Bruce A.
26 REGISTRATION NUMBER: 32,748
27 REFERENCE/DOCKET NUMBER: RAN 6002/170
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (201) 235-5801
30 TELEFAX: (201) 235-2363
31 INFORMATION FOR SEQ ID NO: 8:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 1149 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: double
36 TOPOLOGY: linear
37 MOLECULE TYPE: DNA (genomic)
38 US-09-546-969-8

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Query Match	Similarity	Score	ID#	Length
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Matches 1149	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
QY	1	TCATGCTCTCTCTCTGTGACAGAGGGGGCGTTGGGCGAGGCGACAGCGCTTGCACAGCGG	60	
Db	1149	TCATGCTCTCTCTCTGTGACAGAGGGGGCGTTGGGCGAGGCGACAGCGCTTGCACAGCGG	1090	
QY	61	AATGGGCGGGCGTTCGGGTACGATGCGAAGCCGGTCGGCCAAATTCAAGGGCCCGGCATA	120	
Db	1089	AATGGGCGGGCGTTCGGGTGACGATGCGAAGCCGGTCGGCCAAATTCAAGGGCCCGGCATA	1030	
QY	121	GAAGCGCTCGATCAGGGGGCTGGCGGCAAGCGGGTGAACCGGCTGACGAGGGCGATGCGACG	180	
Db	1029	GAAGCGCTCGATCAGGGGGCTGGCGGCAAGCGGGTGAACCGGCTGACGAGGGCGATGCGACG	970	
QY	181	GTCGGGCGGGCAGCGCGGGAACAGCATTCGGTTTCAGCAGCGCGCAGGAAGCGGTCCGCAATC	240	
Db	969	GTCGGGCGGGCAGCGCGGGAACAGCATTCGGTTTCAGCAGCGCGCAGGAAGCGGTCCGCAATC	910	
QY	241	CGCGCGATCGATGGCCCAAGCCGGCGACCCGGCGCAGCGGGCGGACCGGGTTCGTCAGGTGGCG	300	
Db	909	CGCGCGATCGATGGCCCAAGCCGGCGCACCAGCGCGACCGGGCGGACCGGGTTCGTCAGGTGGCG	850	
QY	301	CGCGCGCATGGCAATCCGCGGCACTGGCGGGGCAATGGGCAAGGGAATATCCGGTGACGGGGTG	360	
Db	849	CGCGCGCATGGCAATCCGCGGCACTGGCGGGGCAATGGGCAAGGGAATATCCGGTGACGGGGTG	790	
QY	361	GAACAGGCTTGGCCCAAGCCCAACCGGCAACCGGCCCTTGGCGGTGTTCGGCGCAGAAAGCC	420	
Db	789	GAACAGGCTTGGCCCAAGCCCAACCGGCAACCGGCCCTTGGCGGTGTTCGGCGCAGAAAGCC	730	
QY	421	TATGGCGTCAATGGGCGCAGCGGATGGGCAAGATGCCCTTTCCGCGCCGCAATCTCTGCCC	480	

Db 729 TATGGGTCATGGGCGACGGCGATGGGCGATGCCCCCTTTGCGCGCATCTCTGCC 670
Qy 481 GGTCCAGCCCCGCTGGCGGCAATGTCAGCGACGGCTGCGCGACGGCCATTCGTCAG 540
Db 669 GGTCCAGCCCCGCTGGCGGCAATGTCAGCGACGGCTGCGCGACGGCCATTCGTCAG 610
Qy 541 ATCGCGCGCGTGGCTGAGCGCGGTATCTCGATCAGATGCGGGTGGACTGAAGGCGAG 600
Db 609 ATCGCGCGCGTGGCTGAGCGCGGTATCTCGATCAGATGCGGGTGGACTGAAGGCGAG 550
Qy 601 CAGATAGATGAAGCGGTATCCGTCCTTCGCGGAAGCGTGGCTGCATGATCATGGGCGG 660
Db 549 CAGATAGATGAAGCGGTATCCGTCCTTCGCGGAAGCGTGGCTGCATGATCATGGGCGG 490
Qy 661 CTGCAAGCATGGGGGCGTCCGCTCGATCTCGATCTGACGCCAGAAATTTCTGGAAGCCAC 720
Db 489 CTGCAAGCATGGGGGCGTCCGCTCGATCTCGATCTGACGCCAGAAATTTCTGGAAGCCAC 430
Qy 721 GGTCAAGTGGCGGGGCTTCAGACGGCACACGGGCGTGCATCAGCGAGCGAGCTCGATCCG 780
Db 429 GGTCAAGTGGCGGGGCTTCAGACGGCACACGGGCGTGCATCAGCGAGCGAGCTCGATCCG 370
Qy 781 CAGAGCGTCCGTCAGCGTGGCGCGCGGTATCTCGATCAGCGCGTGGCAATGGGTATCCACCG 840
Db 369 CAGAGCGTCCGTCAGCGTGGCGCGCGGTATCTCGATCAGCGCGTGGCAATGGGTATCCACCG 310
Qy 841 CAGATGACACCTTGACGACGCCCATGACGCGCGCGCGCTCGATCGACCATAGCGCTGT 900
Db 309 CAGATGACACCTTGACGACGCCCATGACGCGCGCGCGCTCGATCGACCATAGCGCTGT 250
Qy 901 CGTCAAGCGCGCGGAATGCTCGGGAAGCGGACCTTCGTATCGTCCATTCGCGCGGACG 960
Db 249 CGTCAAGCGCGCGGAATGCTCGGGAAGCGGACCTTCGTATCGTCCATTCGCGCGGACG 190
Qy 961 AATGGCGGACAGCGCGCGCGCATTCGCGCGGAAGATCCGTGTGTCGCAAGACCAAGT 1020
Db 189 AATGGCGGACAGCGCGCGCGCATTCGCGCGGAAGATCCGTGTGTCGCAAGACCAAGT 130
Qy 1021 GTGCTGGTCCGAGGGCGGACCGCGCTGAGCATCAGATGCGCGCATCGGCTGCGG 1080
Db 129 GTGCTGGTCCGAGGGCGGACCGCGCTGAGCATCAGATGCGCGCATCGGCTGCGG 70
Qy 1081 GTGCGCAACGGCAAGCGCATGACGCGACCGGACCGCGCGCGCGCGCATGACGAGATC 1140
Db 69 GTGCGCAACGGCAAGCGCATGACGCGACCGGACCGCGCGCGCGCGCATGACGAGATC 10
Qy 1141 ATGGCTCAT 1149
Db 9 ATGGCTCAT 1
RESULT 4
US-09-547-267-8/c
Sequence 8, Application US/09547267
Patent No. 6613543
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Paramontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolpinus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-547-267-8
Query Match 100.0%; Score 1149; DB 4; Length 1149;
Best Local Similarity 100.0%; Pred. No. 1.le-225;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCATGCTCTCTCCGACAGAGGGGCGTTCGCGGCGAGGCGACAGCGCTGCGACAGGCG 60
Db 1149 TCATGCTCTCTCCGACAGAGGGGCGTTCGCGGCGAGGCGACAGCGCTGCGACAGGCG 1090
Qy 61 AATGGCGGCGGCGTCCGCTGACGATGCGAAGCGGTCCGCAATGTACAGCGCGCGGCAATA 120
Db 1089 AATGGCGGCGGCGTCCGCTGACGATGCGAAGCGGTCCGCAATGTACAGCGCGCGGCAATA 1030
Qy 121 GAAAGCGCTGATCAGCGCTGCGGCGAGCGGCTAGAACCGCTGCGACAGCGGCGATGACGAG 180
Db 1029 GAAAGCGCTGATCAGCGCTGCGGCGAGCGGCTAGAACCGCTGCGACAGCGGCGATGACGAG 970
Qy 181 GTGCGGCGGCGGACCGCGGGAACGATCCGGTTCAGCGCGCGGAGGAGCGGTGCGGATC 240
Db 969 GTGCGGCGGCGGACCGCGGGAACGATCCGGTTCAGCGCGCGGAGGAGCGGTGCGGATC 910
Qy 241 CGCGGATGATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 909 CGCGGATGATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 850
Qy 301 CGCGGATGATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 849 CGCGGATGATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 790
Qy 361 GAAAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 789 GAAAGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 730
Qy 421 TATGGCGTCAATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 729 TATGGCGTCAATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 670
Qy 481 GGTCCAGCCCCGCTGGCGGCAATGTCAGCGACGGCTGCGCGACGGCCATTCGTCAG 540
Db 669 GGTCCAGCCCCGCTGGCGGCAATGTCAGCGACGGCTGCGCGACGGCCATTCGTCAG 610
Qy 541 ATCGCGCGCGTGGCTGAGCGCGGTATCTCGATCAGATGCGGGTGGACTGAAGGCGAG 600
Db 609 ATCGCGCGCGTGGCTGAGCGCGGTATCTCGATCAGATGCGGGTGGACTGAAGGCGAG 550
Qy 601 CAGATAGATGAAGCGGTATCCGTCCTTCGCGGAAGCGTGGCTGCATGATCATGGGCGG 660
Db 549 CAGATAGATGAAGCGGTATCCGTCCTTCGCGGAAGCGTGGCTGCATGATCATGGGCGG 490
Qy 661 CTGCAAGCATGGGGGCGTCCGCTCGATCTCGATCTGACGCCAGAAATTTCTGGAAGCCAC 720

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QY      721 GGTCAAGTGGGGGTCTCGACGGCAACCAAGGCGTGAATACGACGACCTCGATCCG 780
Db      429 GGTCAAGTGGGGGTCTCGACGGCAACCAAGGCGTGAATACGACGACCTCGATCCG 370
QY      781 CGAGCCGTCTGACGGCTGCGCCGCTGATCTGACGGCTGCGACATCGTATTCCACG 840
Db      369 CGAGCCGTCTGACGGCTGCGCCGCTGATCTGACGGCTGCGACATCGTATTCCACG 310
QY      841 CAAATGACACCTCTGACGACGCCGATCAGCGCGCCCTCGATGAGACCAAGCTTGT 900
Db      309 CAAATGACACCTCTGACGACGCCGATCAGCGCGCCCTCGATGAGACCAAGCTTGT 250
QY      901 CGTCAAGCGCGCGCAATGCTGGGAAACGCGACCTCTGATCTGATCTGATCTGATCTG 960
Db      249 CGTCAAGCGCGCGCAATGCTGGGAAACGCGACCTCTGATCTGATCTGATCTGATCTG 190
QY      961 AATGGCGACAGCGCGCGCATTCGGCGGAAGATCCGTCTGCTGCGAGGACCAAGT 1020
Db      189 AATGGCGACAGCGCGCGCATTCGGCGGAAGATCCGTCTGCTGCGAGGACCAAGT 130
QY      1021 GTCTGTGCTCGAGGGGCGGACCGCGCTGACGATCAAGATGCGCGCATCCGCTTGG 1080
Db      129 GTCTGTGCTCGAGGGGCGGACCGCGCTGACGATCAAGATGCGCGCATCCGCTTGG 70
QY      1081 GTGCGGAAGCGGCAAGCGCATCAGCGACCGGACGCGCGCGCGCGATTCAGCAATC 1140
Db      69 GTGCGGAAGCGGCAAGCGCATCAGCGACCGGACGCGCGCGCGCGATTCAGCAATC 10
QY      1141 ATGGCTCAT 1149
Db      9 ATGGCTCAT 1

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RESULT 5
US-08-980-832-1
; Sequence 1, Application US/08980832B
; Patent No. 6291204
; GENERAL INFORMATION:
; APPLICANT: Passamonte, Luis
; APPLICANT: Teygakov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/08/980,832B
; CURRENT FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8625
; TYPE: DNA
; ORGANISM: Flavobacterium sp. R1534
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (8348)..(8349)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (8539)..(8540)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (8581)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (8590)
; NAME/KEY: unsure
; LOCATION: (8592)
; NAME/KEY: unsure
; LOCATION: (8602)..(8604)
US-08-980-832-1

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Query Match      100.0%; Score 1149; DB 3; Length 8625;
Best Local Similarity 100.0%; Pred. No. 1.3e-225;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATGCTCTCTCTGAGAGAGGGGGGTTCGGGCAAGGCGGACCGGCTTGACAGCGG 60
Db      5794 TCATGCTCTCTCTGAGAGAGGGGGGTTCGGGCAAGGCGGACCGGCTTGACAGCGG 5853
QY      61 AATGGCGGGGCGTCCGGTGAACGATGCGAAGCCGGTGGGCAATGTGAGGGCGCCGACATA 120
Db      5854 AATGGCGGGGCGTCCGGTGAACGATGCGAAGCCGGTGGGCAATGTGAGGGCGCCGACATA 5913
QY      121 GAAGCGCTGATCAGCGGCTGCGGAGCGGTAGAAACGCTGACAGAGCGATAGCGAGC 180
Db      5914 GAAGCGCTGATCAGCGGCTGCGGAGCGGTAGAAACGCTGACAGAGCGATAGCGAGC 5973
QY      181 GTGGGGCGGGCAGCGCGGGAAGCATTCGGGTTCAGACCGGCAAGAAAGCGGTTCGATC 240
Db      5974 GTGGGGCGGGCAGCGCGGGAAGCATTCGGGTTCAGACCGGCAAGAAAGCGGTTCGATC 6033
QY      241 CGCGCATGATGATGCGCGCAGCGCGGACCGCGGAGCGGAGCGGAGCGGTGTCAGTCCGCG 300
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QY      301 CGCGCGATGATGATGCGCGCAGCGCGGACCGCGGAGCGGAGCGGTGTCAGTCCGCG 360
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Db      6214 TATGGCGTATGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 6273
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QY      601 CAGATGATGAGAGCGGTACCGGTTCATTCGCGGAAACGTCGCGTCCATATATATCGGGCG 660
Db      6394 CAGATGATGAGAGCGGTACCGGTTCATTCGCGGAAACGTCGCGTCCATATATATCGGGCG 6453
QY      661 CTGACGCGCATGGGGGCGTCCGATCTGATCTGACGCGCCAGAAATTTCTGGAACCCAC 720
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QY      721 GGTCAAGTGGGGGTCTCGACGGCAACCAAGGCGTGAATACGACGACGCTCGATCCG 780
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QY      781 CGAGCCGTCTGACGGCTGCGCCGCTGATCTGACGGCTGCGACATCGTATTCCACG 840
Db      6574 CGAGCCGTCTGACGGCTGCGCCGCTGATCTGACGGCTGCGACATCGTATTCCACG 6633
QY      841 CAAATGACACCTCTGACGACGCCGATCAGCGCGCCCTCGATGAGACCAAGCTTGT 900
Db      6634 CAAATGACACCTCTGACGACGCCGATCAGCGCGCCCTCGATGAGACCAAGCTTGT 6693
QY      901 CGTCAAGCGCGCGCAATGCTGGGAAACGCGACCTCTGATCTGATCTGATCTGATCTG 960
Db      6694 CGTCAAGCGCGCGCAATGCTGGGAAACGCGACCTCTGATCTGATCTGATCTGATCTG 6753
QY      961 AATGGCGGACAGCGCGCGCATTCGGCGGAAGATCCGCTGTCAGAGACCAAGT 1020
Db      6754 AATGGCGGACAGCGCGCGCATTCGGCGGAAGATCCGCTGTCAGAGACCAAGT 6813
QY      1021 GTCTGTGCTCGAGGGGCGGACCGGCGCTGACGATCAAGATGCGCGCATCCGCTTGG 1080

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Oy	GTCCGGAACGGCGAACGGCGATCAGCGCACCGGACGCCCGCGCGGATCAGCAGATC	1140
Dd	GTCCGGAACGGCGAACGGCGATCAGCGCACCGGACGCCCGCGCGGATCAGCAGATC	6933
Oy	ATTGCTCAT	1149
Dd	ATTGCTCAT	6942

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, RESULT 6
, US-09-920-923B-1
, Sequence 1, Application US/0920923B
, Patent No. 6677134
, GENERAL INFORMATION:
, APPLICANT: Pasamontes, Luis
, APPLICANT: Tsygankov, Yuri
, TITLE OF INVENTION: Fermentative Carotenoid production
, FILE REFERENCE: 15464 US (C98435/125944)
, CURRENT APPLICATION NUMBER: US/09/920,923B
, CURRENT FILING DATE: 2001-08-02
, PRIOR APPLICATION NUMBER: 08/980,832
, PRIOR FILING DATE: 1997-12-01
, NUMBER OF SEQ ID NOS: 66
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO: 1

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? ORGANISM: Flavobacterium sp. R1534
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (8346)..(8349)
? OTHER INFORMATION: unsure
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (8535)..(8540)
? OTHER INFORMATION: unsure
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (8581)..(8581)
? OTHER INFORMATION: unsure
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (8590)..(8590)
? OTHER INFORMATION: unsure
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (8592)..(8592)
? OTHER INFORMATION: unsure
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (8602)..(8604)
? OTHER INFORMATION: unsure
?
US-09-920-923B-1

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Query Match	100.0%;	Score 1149;	DB 4;	Length 8625;
Best Local Similarity	100.0%;	Pred. No. 1.3e-225;		
Matches 1149; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	TCATCTCTCTCTCTCAGACAGGGGGCGTTCCGGCAGAGGACGACAGGGCTGGACAGCGG	60
Db	5794 TCATCTCTCTCTCTCAGACAGGGGGCGTTCCGGCAGAGGACGACAGGGCTGGACAGCGG	5855
QY	61 AATGGCGCGGGCGTCCCGCTGACGATGCGAAGCGCGTTCGCGCAATGTCAGAGCGCCGGCGATA	120
Db	5854 AATGGCGCGGGCGTCCCGCTGACGATGCGAAGCGCGTTCGCGCAATGTCAGAGCGCCGGCGATA	5913
QY	121 GAAGCGCTCGATCAGCGCGCTGGGGCAGCGCGGTAGAACCGCTTCAGACAGAGCGGATACGACG	180
Db	5914 GAAGCGCTCGATCAGCGCGCTGGGGCAGCGCGGTAGAACCGCTTCAGACAGAGCGGATACGACG	5973

OY	181	GTCCGGGGGGAGCCGGGGAACAGCATCCGGTTACGAGGCCGACGAAAGGGGTGCGCATC	240
Db	5974	GTCCGGGGGGAGCCGGGGAACAGCATCCGGTTACGAGGCCGACGAAAGGGGTGCGCATC	6033
OY	241	CGCCGATTCGATGGCCCGCAGCCGCGCACCGCGCGACCGCGCGGATCGAGGTCCGC	300
Db	6034	CGCCGATTCGATGGCCCGCAGCCGCGCACCGCGCGAGCGCGCGGATCGAGGTCCGC	6093
OY	301	CGCCGCGATGGCGCATCCCGGACCTTCGCGGCGCATTAGGGCAGCGAATATCCGTGACGGGGTG	360
Db	6094	CGCCGCGATGGCATCCCGGACCTTCGCGGCGCATTAGGGCAGCGAATATCCGTGACGGGGTG	6153
OY	361	GAAAGCCCTTGGCCCCCAGCCCCAACCGGACACCGCCCCCTGGCGCGGGGTCCGCCGAAAGCC	420
Db	6154	GAAAGCCCTTGGCCCCCAGCCCCAACCGGACACCGCCCCCTGGCGCGGGGTCCGCCGAAAGCC	6213
OY	421	TATGAGCGCATAGGGCCAGCGCGATAGGGCAGAGATCCCTTTCCGCGCGCATCTTCCTGCC	480
Db	6214	TATGAGCGCATAGGGCCAGCGCGATAGGGCAGAGATCCCTTTCCGCGCGCATCTTCCTGCC	6273
OY	481	GGTCCAGCCCCCGCTGGCGGCGATAGTCCAGGACGCTTGCGCCACGCGCGCATCTTCACG	540
Db	6274	GGTCCAGCCCCCGCTGGCGGCGATAGTCCAGGACGCTTGCGCCACGCGCGCATCTTCACG	6333
OY	541	ATCCCGCCGCTCGCTTGATAGCGCGGATCTCTCGATACAGATCGGGGTGGGACTGAAGGGCAG	600
Db	6334	ATCCCGCCGCTCGCTTGATAGCGCGGATCTCTCGATACAGATCGGGGTGGGACTGAAGGGCAG	6393
OY	601	CAGATTAGTAGAAGCGGATACCCGTCATCTGGCGGAACGGTCCGCTCCATATCATCGGAGC	660
Db	6334	CAGATTAGTAGAAGCGGATACCCGTCATCTGGCGGAACGGTCCGCTCCATATCATCGGAGC	6453
OY	661	CTCGACGCCATGGGGGGGCGTGGTCTCGATCTCGACGCCCCACGAAATTTCTGGAAACCCAC	720
Db	6454	CTCGACGCCATGGGGGGGCGTGGTCTCGATCTCGACGCCCCACGAAATTTCTGGAAACCCAC	6513
OY	721	GGTCAAGGTGGGGGTCTTCGACCGGACCAACCGGCGCTCGATACAGGAGCAGCGTCGATCCG	780
Db	6514	GGTCAAGGTGGGGGTCTTCGACCGGACCAACCGGCGCTCGATACAGGAGCAGCGTCGATCCG	6573
OY	781	CGAGCCGTCGTCGACGCGTCGCGCGGGTATCGTCCAGCGTCGACGATGCGTATTCACACG	840
Db	6574	CGAGCCGTCGTCGACGCGTCGCGCGGGTATCGTCCAGCGTCGACGATGCGTATTCACACG	6633
OY	841	CAGATTCGACACCTTCGACGACAGCCCGATCAAGCGCGCCGCGCTCGATCGAACCCATAGCTGT	900
Db	6634	CAGATTCGACACCTTCGACGACAGCCCGATCAAGCGCGCCGCGCTCGATCGAACCCATAGCTGT	6693
OY	901	CGTCAAGCGCGCGCGCAATGTGTGGGAAACCGGACCTCTGATCCGTCCATTTCGCCCGACG	960
Db	6694	CGTCAAGCGCGCGCGCAATGTGTGGGAAACCGGACCTCTGATCCGTCCATTTCGCCCGACG	6753
OY	961	AATGGGGCGACGGGGGCGCCAGCCCATTTGGGGGAAAGATCCGTGTGTGGCGACGACAGT	1020
Db	6754	AATGGGGCGACGGGGGCGCCAGCCCATTTGGGGGAAAGATCCGTGTGTGGCGACGACAGT	6813
OY	1021	GTGCTGTGTCGAGGGGCGCGGACCGCGCGTCGAGCATCAAGATGCCGCAATCCGTTCCG	1080
Db	6814	GTGCTGTGTCGAGGGGCGCGGACCGCGCGTCGAGCATCAAGATGGCGCGATCCGTTCCG	6873
OY	1081	GTCGCGAAGCGGCAAGCGCGATCAGCGCACCGGACAGCCCGCGCGCGCATCAGCAGATC	1140
Db	6874	GTCGCGAAGCGGCAAGCGCGATCAGCGCACCGGACAGCCCGCGCGCGCATCAGCAGATC	6933
OY	1141	ATGGCTCAT 1149	
Db	6934	ATGGCTCAT 6942	

RESULT 7
US-08-980-832-27
; Sequence 27, Application US/08980832B
; Patent No. 6291204

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; GENERAL INFORMATION:
; APPLICANT: Paramontes, Luis
; TITLE OF INVENTION: Improved Fermentative Carotenoid Production
; FILE REFERENCE: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/08/980,832B
; FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11233
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Plasmid pZee4
US-08-980-832-27

Query Match      100.0%; Score 1149; DB 3; Length 11233;
Best Local Similarity 100.0%; Pred. No. 1.4e-225;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATGCTCTCTCTGAGAGAGGGGGCGTTGCGGAGGAGCGGAGCGGCTTGCAGACGG 60
DB      6476 TCATGCTCTCTCTGAGAGAGGGGGCGTTGCGGAGGAGCGGAGCGGCTTGCAGACGG 6535
QY      61 AATGGGCGGGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB      6536 AATGGGCGGGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6595
QY      121 GAAGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
DB      6596 GAAGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6655
QY      181 GTGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 240
DB      6656 GTGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 6715
QY      241 CGCGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB      6716 CGCGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6775
QY      301 CGCGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB      6776 CGCGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6835
QY      361 GAACAGCCCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 420
DB      6836 GAACAGCCCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 6895
QY      421 TATGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB      6896 TATGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6955
QY      481 GGTCAGCGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
DB      6956 GGTCAGCGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7015
QY      541 ATCGCGCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
DB      7016 ATCGCGCGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7075
QY      601 CAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB      7076 CAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7135
QY      661 CTCGAGCGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
DB      7136 CTCGAGCGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7195
QY      721 GGTGAGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
DB      7196 GGTGAGGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7255

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QY      781 CGAGCGCTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB      7256 CGAGCGCTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 7315
QY      841 CAGATGACACCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB      7316 CAGATGACACCTTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7375
QY      901 CGTCAGCGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB      7376 CGTCAGCGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7435
QY      961 AATGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
DB      7436 AATGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7495
QY      1021 GTGCTGCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
DB      7496 GTGCTGCTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7555
QY      1081 GTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
DB      7556 GTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7615
QY      1141 ATGGCTCAT 1149
DB      7616 ATGGCTCAT 7624

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RESULT 8
US-09-920-923B-27
; Sequence 27, Application US/09920923B
; Patent No. 6677134
; GENERAL INFORMATION:
; APPLICANT: Paramontes, Luis
; APPLICANT: Teygankov, Yuri
; TITLE OF INVENTION: Fermentative Carotenoid Production
; FILE REFERENCE: 15464 US (C39435/125944)
; CURRENT APPLICATION NUMBER: US/09/920,923B
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 08/980,832
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 11233
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Plasmid pZee4
US-09-920-923B-27

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Query Match      100.0%; Score 1149; DB 4; Length 11233;
Best Local Similarity 100.0%; Pred. No. 1.4e-225;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATGCTCTCTCTGAGAGAGGGGCGTTGCGGAGGAGCGGAGCGGCTTGCAGACGG 60
DB      6476 TCATGCTCTCTCTGAGAGAGGGGCGTTGCGGAGGAGCGGAGCGGCTTGCAGACGG 6535
QY      61 AATGGGCGGGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB      6536 AATGGGCGGGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6595
QY      121 GAAGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB      6596 GAAGCGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6655
QY      181 GTGCGGCGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB      6656 GTGCGGCGGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6715
QY      241 CGCGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300

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6716 CCGCGATGATGCGCCAGCCCGCGCAGCCCGCGAGCGCGGTGATGAGGTGCGG 6775
QY 301 CCGCGGATGATGCGCGGCGCGGCGGATGAGGCGAGGATATCCGGTGAAGCGGCG 360
DB 6776 CCGCGGATGAGGATCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 6835
QY 361 GAACAGCCCTGCGCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 420
DB 6836 GAACAGCCCTGCGCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 6895
QY 421 TATGCGGTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 6896 TATGCGGTATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6955
QY 481 GGTCCAGCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 540
DB 6956 GGTCCAGCCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 7015
QY 541 ATGCGCGCGCGGTGCGGTGCGGTATCTGATGATGAGGCGGCGGCGGCGGCGGCGG 600
DB 7016 ATGCGCGCGCGGTGCGGTGCGGTATCTGATGATGAGGCGGCGGCGGCGGCGGCGG 7075
QY 601 CAGATGATGAAAGCGGTATCCCGTCCATCTGCGGAAAGCGTCCGATGATGATGCGGCG 660
DB 7076 CAGATGATGAAAGCGGTATCCCGTCCATCTGCGGAAAGCGTCCGATGATGATGCGGCG 7135
QY 661 CTGCGCGCGCGGTGCGGTGCGGTATCTGATGATGAGGCGGCGGCGGCGGCGGCGG 720
DB 7136 CTGCGCGCGCGGTGCGGTGCGGTATCTGATGATGAGGCGGCGGCGGCGGCGGCGG 7195
QY 721 GGTGAGGTGCGGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 780
DB 7196 GGTGAGGTGCGGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 7255
QY 781 CGAGCGGTGCGGTGCGGTGCGGTATCTGATGATGAGGCGGCGGCGGCGGCGGCGG 840
DB 7256 CGAGCGGTGCGGTGCGGTGCGGTATCTGATGATGAGGCGGCGGCGGCGGCGGCGG 7315
QY 841 CAGATGATGAAAGCGGTATCCCGTCCATCTGCGGAAAGCGTCCGATGATGATGCGGCG 900
DB 7316 CAGATGATGAAAGCGGTATCCCGTCCATCTGCGGAAAGCGTCCGATGATGATGCGGCG 7375
QY 901 CGTCAAGCGGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
DB 7376 CGTCAAGCGGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 7435
QY 961 AATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1020
DB 7436 AATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7495
QY 1021 GGTGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
DB 7496 GGTGCGGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7555
QY 1081 GTGCGGAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
DB 7556 GTGCGGAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 7615
QY 1141 ATGCGGTGAT 1149
DB 7616 ATGCGGTGAT 7624

RESULT 9
US-08-663-310-5/c
; Sequence 5, Application US/08663310
; Patent No. 5811273
; GENERAL INFORMATION:
; APPLICANT: MISAWA, No. 5811273hiko
; APPLICANT: KONDO, Keiji
; APPLICANT: KAWIMURA, Susumu
; APPLICANT: YOKOYAMA, Akihito

|||||
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1161 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1158
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..1158
US-08-663-310-5
Query Match 55.8%; Score 640.8; DB 1; Length 1161;
Best Local Similarity 73.4%; Pred. No. 5,6e-122; Indels 12; Gaps 2;
Matches 851; Conservative 0; Mismatches 297;
QY 1 TCATGCTCTCTCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
DB 1161 TCATGCTCTCTCTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1102
QY 61 AATGCGCGGCGGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 120
DB 1101 AATGCGAGGCGTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1042
QY 121 GAAGCGGTGATGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 180
DB 1041 GAAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 982
QY 181 GTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 981 GTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 922
QY 241 CCGCGGATGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 294

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Db      921 CGCCCGATCGATCGCTAAATCGCGATGCGCGCCGACGCGTCCGTCCGCGCGCGCGCC 862
Qy      295 GTGCGCGCGCGATGCGATCCCGCACTGCGCGGATAGGGAGGAATATCCGCTGC 354
Db      861 GGAACAACCCGACCACTGCGCGCACTGTGCGATAGGGAGGAATAGCGGTGAC 802
Qy      355 GGGGTGAACAGCCCTGCGCCGACCAACCGGACCGCCCTGCGGTGTCGCGCA 414
Db      801 CGGATGAAGAACCCCGCGCGAGTCCACGGAACAGGCCCGCGCGATCGGCCA 742
Qy      415 GAAGCTATGCGCTCATGCGCCAGCGCGATGCGGAGATGCCCTTTCCGCGCATCTC 474
Db      741 GAAGCCCGCGCATCATGCGCCAGCGCGATGCGGAAGATGCCGCTTCCGCGCATCTC 682
Qy      475 CTGCGCGGTGCGAGCCCGCTGCGCGCATGATGCGACGCGCTGCGCGAGCGCGCATC 534
Db      681 GGGCCCGGTGCGAGCCCTGCTGCGGCGATGATGTGGAAGCGCGCGCGCGCGCGTCTG 622
Qy      535 GTCCAGATGCGCGCGCTGCTGAGCGCGATCTCGATCAGGATCGGGTGGACTGA 594
Db      621 GTCCAGATGCGCGCGCATCGGAATAGCGCGTCTCTGATCAGGATCGCGTCCGAGAGA 562
Qy      595 GGGCAGCAGATGATGAAGCGGTACCCGTCATCTGCGGAACGTCGCGTCCATGATCAT 654
Db      561 GGGCAGCAGATGATGAAGCGGTACCCGTCCTGCGGTGACGCGTCCGTCATGATCAT 502
Qy      655 CGGCGCTGCGAGCCCATGCGGGCGCGTCTGTCATCTGACGCCCAAGAAATTTCTGGA 714
Db      501 CGGCGCGGCGACCCGTCGGGGCGGTGCGTCTGATCTGACACCCAGAAATTTCTGGA 442
Qy      715 ACCCAGCTGAGGTGCGGGGTCGACGCGACCGAGGCGTCGATCAGCAGGACGCTC 774
Db      441 ACCCAGCTGAGGTGCGGGGTCGCGAGCGGTGCGCGCGCGCGCGCTCCAGAGACGCGCGCTC 382
Qy      775 GATCCCGAGCGCTCCGTCAGCGTCGCGCGGTATCTGTCAGCGTCCGATCGCTATT 834
Db      381 GATCCCGAGGTGCGCGAGAGAGCGTCGCGCGCTCCGATCAGAGGCGCATGTCGCTGTC 322
Qy      835 CCACCGCAGATGCAACCTCTGACGACG-----CCGATCAGCGCGCGCGCTCTGATCCA 888
Db      321 CCACCGCAGATCTCGCGCGCGCGACCGACACCGCATCCGCGAGCGCGCGCGCTCTGACGCA 262
Qy      889 GCGATGCTGCTGTCAGAGCGCGCGAATGATGCGGAAACGCGACCTCTGATCCGTCCA 948
Db      261 CCGTAACTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 202
Qy      949 TTCGCGCGCAGATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1008
Db      201 GTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 142
Qy      1009 GCGAGACCGGTGCTGCTGCTGCGAGGGGCGCGACCGCGCGTCCAGCATCAGATGCGCGC 1068
Db      141 GCGAGACCGGTGCTGCTGCTGCGAGGGGCGCGACCGCGCGTCCAGCATCAGATGCGCGC 82
Qy      1069 ATCCGCTGCGCGTCCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1128
Db      81 GTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22
Qy      1129 GATCAGCAGATCATGCTCA 1148
Db      21 CAGCAGCAGATCATGCTCA 2

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; TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,491
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/663,310
; FILING DATE: 23-SEP-1996
; APPLICATION NUMBER: WO PCT/JP94/02220
; FILING DATE: 26-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-235917
; FILING DATE: 05-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-348737
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 49441/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1158
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 1..1158
; US-09-006-491-5
;
Query Match      55.8%; Score 640.8; DB 2; Length 1161;
Best Local Similarity 73.4%; Pred. No. 5,6e-122;
Matches 851; Conservative 0; Mismatches 297; Indels 12; Gaps 2;
;
Qy      1 TATGTCCTCTCTGACGAGAGGGGCGCTTGGGCGAGCGCGCGCTGCGAGACGCG 60
Db      1161 TATGTCCTCTCTTCTTCAAGAGGAGGCTTGGGCGAGCGCGCGCTGCGAGAGG 1102
Qy      61 AATGGGCGGGCGCTGCGGTGACGATGCGAGAGCGGTCGCGCAATGTCTAGAGCGCGCGCAT 120
Db      1101 AATGGAGGCTTGGCGGTGACGATGCGAGAGCGGTCGCGCAATGTCTAGAGCGCGCGCAT 1042
Qy      121 GAAGCGCTGATCAGCGCGCTGCGGAGCGGTGAGAACCGCTGCGACGAGCGATAGCGAGC 180
Db      1041 GAACGCTGATCAGTCATGCGGATGCGGTAGAACCGCTGCGACGAGGATATAGCGCGC 982
Qy      181 GTGCGCGCGCGCGCGCGCGAGACGATCGGTTTCAGCAGCCCGCAGAGAGCGGTCCGATC 240
Db      981 GTGCGCGCGCGCGCGCGCGAGACGATCGGTTTCAAAAGCGCGCAAAAGCGGTCCGCGCG 922
Qy      241 CCGCGATGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 294

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Db      921  CGCCCGGTCGATCGCGTATATGCGGATGAGCGCCCGCGCAGCGCGTCCGGTCCGGCCGGCC 862
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Db      861  GGAAGAACCCCGCCACACAGTCCGCACTGTGCGCATATAGGGCAGCGAATAGCCGGTGAC 802
QY      355  GGGGTGAAACACCCCTGCCCCCAGCCCAACCGGCAACCGCCCCCTCCGCTGTGTGTGGCCCA 414
Db      801  CGGATGAAAGAACCCCGCGCGCAGTCCCAAGGAAACAGTCCCGCGCGGTGATGAGCCCA 742
QY      415  GAAGCGTATGAGCGTCAATGGGCGCAGCGCATGGGAGAGATGCCCTTTTCGCGCGCATCTC 474
Db      741  GAAAGCCCGCCGATCATATGGGCCAGCGCATGGGAAAGATGCCGGTTCGCGCCGGACTC 682
QY      475  CTGCCCCGGTCAGCCCCCGCGCTTGGCGGCAATGATCCAGCGACGCGCTTGCAGCGCGCATC 534
Db      681  GAGCCCGGATCAGCCCTGCTGGCGGGCATGATGCTGTGGGACCGCCCGCCAGCGCGTGTCT 622
QY      535  GTCCAGATACCGCGCGCGTGCCTGTAGCGCGGTATTCCTCAGATCAAGATATCGCGGGGAACTGAA 594
Db      621  GTCCAGATACCGCGCGCATGGAATAGCGCGGTGTCTTCGATCAAGATATGCGCGCGTGAAGAA 562
QY      595  GGGCAGCAGATAGATGAAGCGGTACCCGCTCATCTTGCAGGAACGGTGCCTCATATCAT 654
Db      561  GGGCAGCAGATAGATGAAGCGGTACCCGCTCTGCTGGGTGACGGTCCGCTCATATCAT 502
QY      655  CGGGCGCTCGACGCCATGGGGGGCGTCCGATCTCGATCTCGACGCCCAAGAAATTTCTGAA 714
Db      501  CGGGGGGGGACCGCGGTGGGGGGCGGTCCGATCTCGATCTCGACCAACAGAAATTTCTGAA 442
QY      715  ACCCAGCGTCAAGTACGGGGGTCTCGACCGGCACACAGGGCGTTCGATCAACGAGGACGCTC 774
Db      441  ACCCAGCGTCAAGATGCCCGCAACGGCTGCGCGCCCGCGCTTCAGGAACCGCGCGCTTC 382
QY      775  GATCCGCGAGCGCGTCCGTCAAGCGTACGCGCGGTATCGTCCAGCGTCCGCAATCGATATT 834
Db      381  GATCCGCGGTCCGAGGACAGCGGTCCCGCTCGCGCATCCAGGAGGAGATGTCCGTCTC 322
QY      835  CCACCGCAGATCGACACCCCTGCAGCAGC-----CCGATCAAGCGCGCCCGCGCTCGATCGA 888
Db      321  CCAGCGGATCTCCGGCGCCCGACCGGACCAACGCGATCCGCGCAGCGCGCGCCCGTCAAGGA 262
QY      889  GCCATAGCGCTGTCCGTCAAGCGCGCGCGAATGCTCGGAAACCGGACCTTCTATCTCTTCA 948
Db      261  CCGGTAAACCGGTGGCGCAGCGCGCGCGGCGATGCGGGGAAAGCGCACTTCTCTGTACGGGCA 202
QY      949  TTCCGCGGAGAGGAATGGGCGGACAGCGCGGCGCAGCGCATTTCCGGCGGAAAGATCCGTGTCTG 1008
Db      201  GTTGGCGGCGCGCAGGGGCTTCAAGCGCGGCGCAGCGCATGTCGCGCAGCAGGTGGGGTCTGT 142
QY      1009  GCAGGACCAAGGTGTGCTGTCTCGAAGGGGCGCGAACCGCGCGTTCAGGACATCAAGATGCGCGC 1068
Db      141  GCAGGACCAAGGTGTGCGCGTCTGACAGGTCTTGCGCGCATGTCTCAGCAGCAGCAGCGCAG 82
QY      1069  ATCCGCTTTCGCGTTCGCGTTCGCGAACGCGAAGCGCGATCAAGCGCACCGACCGCGCGCCG 1128
Db      81  GTCCGGCGCGCGCGCGCGCAGCGCCAGGGCGATCAGCCGTTTGGCAAGGCCCGCGCCCTGC 22
QY      1129  GATCAGCAGATCATGGCTCA 1148
Db      21  CAGCAGCAGTCATAGGTCA 2

RESULT 11
US-09-335-919-5/C
; Sequence 5, Application US/09335919
; Patent No. 6150130
; GENERAL INFORMATION:
; APPLICANT: MISAWA, No. 6150130@hiko
; APPLICANT: KONDO, Keiji
; APPLICANT: KAJIWARA, Susumu
; APPLICANT: YOKOYAMA, Akihiko
;

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1 TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
2 TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
3 TITLE OF INVENTION: XANTHOPHYLLS
4 NUMBER OF SEQUENCES: 12
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Foley & Lardner
7 STREET: 3000 K Street, N.W., Suite 500
8 CITY: Washington
9 STATE: D.C.
10 COUNTRY: USA
11 ZIP: 20007-5109
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patentin Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/09/335,919
19 FILING DATE:
20 CLASSIFICATION:
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US/08/663,310
23 FILING DATE: 23-SEP-1996
24 APPLICATION NUMBER: WO PCT/JP94/02220
25 FILING DATE: 26-DEC-1994
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: JP 6-235917
28 FILING DATE: 05-SEP-1994
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: JP 5-348737
31 FILING DATE: 27-DEC-1993
32 ATTORNEY/AGENT INFORMATION:
33 NAME: BENT, Stephen A.
34 REGISTRATION NUMBER: 29,768
35 REFERENCE/DOCKET NUMBER: 49441/109
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (202)672-5300
38 TELEFAX: (202)672-5399
39 TELEX: 904136
40 INFORMATION FOR SEQ ID NO: 5:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 1161 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: double
45 TOPOLOGY: linear
46 FEATURE:
47 NAME/KEY: CDS
48 LOCATION: 1..1158
49 FEATURE:
50 NAME/KEY: mat_peptide
51 LOCATION: 1..1158
52 US-09-335-919-5
53
54 Query Match 55.8%; Score 640.8; DB 3; Length 1161;
55 Best Local Similarity 73.4%; Pred. No. 5.6e-122;
56 Matches 851; Conservative 0; Mismatches 297; Indels 12; Gaps 2
57
58 1 TCATGCTCTCCGTCGACGACGAGGCGGCTTGGGAGGAGGCGCA CGGCGTCGACAGCGG
59
60 1161 TCATGCGCTTTCTCTTCACGAGGAGCGTTCGAGGACGACGCGATGCGCTCCAGAGG 1107
61 AATGGGCGGGCGCTCCGCTGACGATGCGAAGCGCGGTGCGCAATGTCAAGCGCCGCGCAT 120
62
63 1101 AATGGAGAGCGTTGGCGCGTCAAGATGCGGAGCTGATCCGCCA GCGTCACCGCGCGCAT 104
64
65 121 GAAGCGCTCGATCAGCGGCTGCGGACGCGGCTAGAACCGCTGACAGCGCGATTAACGAC 180
66
67 1041 GAACCGTTGATCAGTCAGTCATCCATCCAGCGGACATGCGTAGAACCGCTGACGACGAGGTTATGACGCGC 982
68
69 181 GTCGGCGCGGAGCGCGCGGAAACAGCATCCGGTTTCACGACGCGCGAGGAAGCGGTGCGCATC 240
70
71 981 GTCGGGCGCGAGCGCGGAAACAGCATCCGGTTTCACGAGGCGCGAGGAAGCGGTGCGCGCG 922

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OY	241	CGCGGATATCGATGGCCCAAGCCGCGACCGCGGACG-----GGCGGAAAGCGGATGCTGAC	294
Db	921	CGCCCGGTGATCGCGTATCGCGATGCGCGCGCGCGACGCGGTGCGTCCGCGCGGCC	862
OY	295	GTGCGCGCGCGGATGCGATCCGCGACCTTGCAGCATATGAGGACAGCGAATATCCGTGAC	354
Db	861	GGAACGACCCGCCCAACAAGTCCGACCTGTGCGCGATAGGGCAAGGAATACCGGTGAC	802
OY	355	GGGGTGGAAACAGCCTTGCCCCAGCCCAACCGGACACGCGCCCTTGCGGTGGTCCGCA	414
Db	801	CGGAAGAAAGAACCCCGCGCGCATGCCACGGGAAAGAGCCCGCGCGCTGATCGGCCA	742
OY	415	GAAGCCTATGGCGTCATGGAGGCGAGCGCGATGGGACGATGAGCCCTTTGCGCGCGCATTC	474
Db	741	GAAGCTCCCGCGCATATGGGCCAGCGCGCATGGGAAAGATCCGCTTTCGCGCGACCTC	682
OY	475	CTGCGCGGTCCAGCCCGCGCTTGCGCGCATATGTCAGACGACGCTTGCGCGACGCGCATC	534
Db	681	GGCCCGGTCAGCCCTTGCGCGGCGCATATGTCATGGAGCGCGCGCGCGCGGTGCTC	622
OY	535	GTCCAGATCGCCGCGGTGCTGTAGCGGTATCTCGATCAGGATGCGGGTGGACTGA	594
Db	621	GTCCAGATCGCCGCGCATCGAATAACGCGTGTCTTCGATCAAGATGCGCGTGGAGAGA	562
OY	595	GGGCGACGATATGATGAAGCGGTACCCGTCATCTGCGGAAAGGTGCGGTCCATATCAT	654
Db	561	GGGCGACGATATGATGAAGCGGTACCCGTCGCTGGGGTAGCGGTGCGCTTCATATCAT	502
OY	655	CGGGCGCTCGACGCCATGGGGGCGCTCGGTCTCGATCTCGACGCCACGAATTTCTGAA	714
Db	501	CGGGCGGGGCAAGCGGTGGGGCGGTGGTCTCGATCTCGAACCCACGAATTTCTGAA	442
OY	715	AACCCAGGTCAAGGTGCGGGGTCTCGACGGCACACGGGCGTCTGATCAGCAGGACAGCTC	774
Db	441	AACCCAGGTCAAGATCCGCGACGGGCTGGCGCCCGCGCTTCAGAGACCGCGCGCTC	382
OY	775	GATCCGCGAGCGCTCGGTACAGCGTGGCGCGGTATCTGTCACAGTTCGAGCAATGGGTAT	834
Db	381	GATCCGCGGTGCGCGAGAACGCGTGGCCCCCTGCGCATTCACAGGCGCATGTGCTGTC	322
OY	835	CCACCGCATTCGACACCTTGACAGAC-----CCGATCAGCGCGCGCGCTTCATCGA	888
Db	321	CCAAGGATCTCGCGCGCTCGAACCGAACCAACCGCATTCGCGAGCGCGCCCGTCCAGCA	262
OY	889	GCCATAGCCTGTCTGTCAGCGCGCGCGAATGTCGAGAAACGCGACTTCTGATCCGTCA	948
Db	261	CCCGTAACGGGTGGCCAGCGCGCGCGGATAGCGGGGAAAGCGACCTCTGTGTCGAGCA	202
OY	949	TTCCGCGCGGACGAATGGGCGACAGCGCGCGCGACCATTCGCGCGGAAAGATCCGTGCTG	1000
Db	201	GTGGCGCGGCGCAGAGGGCTTTCAGCTCGCGCGACGATCCGCGACAGGTCGGGTCTGTG	142
OY	1009	GCAGGACAGGATGTCGTGTCGAGAGGGCGCGACCGCGTGCAGCATACAGATCGCGAC	1066
Db	141	GCAGGACAGGATGTCGTGTCGAGAGGCTGACAGGTCTTCGCGCATGTCTCAGCAGCAGACGCGACG	82
OY	1069	ATCCGCTTGGCGTTCGCGAACGGCAAGCGCGATTCAGCGCACCGACAGCCCGCGCGC	1122
Db	81	GTGGGGCGCGCCGCGCGCAGCGCGCATGACCGCTTGGCAAGGCGCGCCCTGTC	22
OY	1129	GATCAGCAGATCATATGGCTCA	1148
Db	21	CAGCAGCAGTCAATGGGTCA	2

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RESULT:2
US-08-663-310-7/c
; Sequence 7, Application US/08663310
; Patent No. 5811273
; GENERAL INFORMATION:
; APPLICANT: MITSUBI, Keiichi
; APPLICANT: KONDO, Katsuhiko
; APPLICANT: KAJIWARA, Susumu

```

```

? APPLICANT: YOKOYAMA, Akihito
? TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
? TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
? TITLE OF INVENTION: XANTHOPHYLLS
? NUMBER OF SEQUENCES: 12
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley & Lardner
? STREET: 3000 K Street, N.W., Suite 500
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20007-5109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/663,310
? FILING DATE: 23-SEP-1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/JP94/02220
? FILING DATE: 26-DEC-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: JP 6-235917
? FILING DATE: 05-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: JP 5-348737
? FILING DATE: 27-DEC-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A.
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 49441/109
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 672-5300
? TELEFAX: (202) 672-5399
? TELEX: 904136
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2886 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
?
? US-08-663-310-7
?
Query Match 55.8%; Score 640.8; DB 1; Length 2886;
Best Local Similarity 73.4%; Pred. No. 6.1e-12;
Matches 851; Conservative 0; Mismatches 237; Indels 12; Gaps 2;
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Db 2509 TCATGCGTTTCTTCAACAGAGGAGCACTTGGCGAGGCAAGGATGCGCTGCCAAGGG 2450
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QY 61 AATGGGCGGGCGTCGCGTGAACGATGCGAAGCGGTCGCGCAATGTCAAGGCGCCGCGATA 120
Db 2509 TCATGCGTTTCTTCAACAGAGGAGCACTTGGCGAGGCAAGGATGCGCTGCCAAGGG 2450
?
Db 2449 AATGGAGAGGCTTGGCGGTCAAGATGCGCAGCTGATCCGCAACGCTCAGCGCGCGGATA 2390
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QY 121 GAAGCGCTCGATCAGCGCGCTGCGGCGAGCGGTAGAACCGCTGCGAGCGAGCGCATGCGACG 180
Db 2389 GAACCGTTTCATCATGTCATGTCGCGCATGCGGATGAGAACCGCTGCGACAGGCTATGCGCG 2330
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QY 181 GTCGGGCGGGCAGCGCGGGAACAGCATTCGAGTTTCAAGACGCGCAGAAAGCGATCGCATC 240
Db 2329 GTCGGGCGGGCAGCGCGGGAACAGCATTCGAGTTTCAAGAAAGCGCAGAAAGCGATCGCGG 2270
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QY 241 CGCGCATGATGAGCGCCAGCGCGCGACCGCGCGACG-----GGCGGACGCGGTGCTAG 294
Db 2269 CGCGCGGTGATCGCGTAATCGGGAATGCGGATGCGCGCGCGACGCGCGTGGTGGCGGCGGCC 2210
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QY 295 GTGCGGCGCGCGCATGCGCATTCGCGAAGCTGCGCGCGCATTAAGGCGAGCGGAATATCCGATGAC 354
Db 2209 GAGACGACCGCGCACACGTCCTCGCACTTGTCGCGCATTAAGGCGAGCGGAATATGCGGATGAC 2150

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OY	355	GGGGTGAAGAACGCCCTGCGCCCCAGCCCAACCGGACCGCCCTCGCGCGTGTGTGCGCGCA	414
Db	2149	CGGATGAAAGAACCCCCGCGCGCATGTCCACGGGAACAGGCCCCCGCGGTATGGGCCCA	2090
OY	415	GAAGCTATGGCGTTCATGGAGGCGCAGCGCGATGGAGAGATGCCCTTTGCGCGCATCTC	474
Db	2089	GAAGCCCGCGCATCATGGGCGAGCGCATGGGAAGATGCGCGGTTGCGCCGGACCTC	2030
OY	475	CTGCGCCGGTCCAGCCCGCCCTGAGCGGCAATAGTCCAGGCAAGCCCTGCGCLACCGGCATC	534
Db	2029	GGCCCCGGGTTCAGCCCTCTGTGCGGGACATAGTCTGGGAGCCCGCGCACGGCGTGTCTC	1970
OY	535	GTCCGAGATCGCGCGCCGTGCTGTAGCGCGGTATCCCTCATACAGAAATGCGGGTGGGACTGAA	594
Db	1969	GTCCAGATCGCGCGCATCATGGAAATAGCGGTGTCTCTCATACAGATTCGCGCTCGAGAGAA	1910
OY	595	GGCGCAGCATAGATGAAGCGGTACCCGTTCATCTGCGAAACGGTTCGGTCCATGATCAT	654
Db	1909	GGGCGAGCATAGATGAAGCGGTACCCGTCTGCTGGGTGACGGTTCGGTCCATGATCAT	1850
OY	655	CGGGGCGTCCAGCGCATAGGGGGGGCGTGGGTCTCATCTTCAGACGCCCAAGATTTCTGGAA	714
Db	1849	CGGGGCGGCGCAGCGGTGGGGGGCGTGGGTCTCATCTTCAGACCCCAAGATTTCTGGAA	1790
OY	715	ACCCACGGTTCAGAGTGCAGGGGTCTCGACAGCGCAACAAGGGCGTTCAGATCAAGCAGCAGCTTC	774
Db	1789	ACCCACGGTTCAGATTCGCCCGCAACGGTGGCGGCCCGCGCCGTTCAGAACCGGCGCCGTTC	1730
OY	775	GATCCGCGAGCCGTTCGTAGCGTTCGCGCGGGATCGTTCAGACGTTCGCGCATGCGTATT	834
Db	1729	GATCCGCGGTGCGCGCAGGACAGCGTTCGCCCTCGCGCATTCAGCAGGGCGATGTGCTGTCTC	1670
OY	835	CCACCGCAGATTCAGACCCCTGAGCAGC-----CCGATTCAGCGCGCCCGCTCGATCGA	888
Db	1669	CCAGCGGATCTTCGAGCGCCCAACCGGACCAACGCGATTCGCCAGCGCGCGCCGTTCAGCGA	1610
OY	889	GCCATAGCCTGTCTGTACAGCGCGCGCGAATGTCGGGAAACCGCATCTTCTGATCCGTTCGA	948
Db	1609	CCCGTACCGGTGGGCGCAACCGCGCGGAGATGGGGGGAAGGCACTCTCTGTGGGGCA	1550
OY	949	TTCCGCCGCGACGATGGGCGACAGCGCGCGCACGCCATTCGGGCGGAAGATCCGTGTCTGT	1008
Db	1549	GTTGGCGCGCGCGCAGGGGCTTTCAGCGCGCGCACCGCATGTCCGCGACAGGTGGGGTCTGT	1490
OY	1009	GCAGGACGAGGTGTCTGTCTCGAGGGGCGCGAACCGCGCGTTCGACATCAGATGGCGCGC	1068
Db	1489	GCAGGACGAGGTGTGTGCGGTCTGAGAGGTCTGCGCGCATGTTCAGACACAGCAACGCGAG	1430
OY	1069	ATCCGCTGTGCGGTGCGGACAGCGCAGCGCATACGCCACCGGACAGCCCGCGCGCCGC	1128
Db	1429	GTCGGGGCGCGCGCGCGCGACGCGGCGGCGATGAGCCCGTTGGGAAGCCCGCGCCCTG	1370
OY	1129	GATCAGCAGATCATGGCTCA	1148
Db	1369	CAGCAGCACGTTCATGGTCA	1350
RESULT 13			
US-09-006-491-7/c			
; Sequence 7, Application US/09006491			
; Patent No. 5972690			
; GENERAL INFORMATION:			
; APPLICANT: MISAWA, No. 5972690ihiko			
; APPLICANT: KONDO, Keiji			
; APPLICANT: KAJIWARA, Susumu			
; APPLICANT: YOKOYAMA, Akihiro			
; TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF			
; TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE			
; NUMBER OF SEQUENCES: 12			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Foley & Lardner			

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,491
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2886 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: linear
US-09-006-491-7

Query	March	Similarity	55.8%	Score	640.8	DB	2	Length	2886
Best Local Match	851	Conservative	73.4%	Pred.	No. 6.1e-122	Mismatches	0	Indels	12
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QY	1	TCATGCTCTCTCTGTGACAGAGGGGCGTTCGGGACAGGACGGCGCATGCGACAGCGG							60
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QY	61	AATGGGCGGGCGTCCGGTGAAGATGCCAAGCCGCTCCGGCCAAATTCAAGCGCCCGGCATA							120
Db	2449	AATGGAGGCTTGGCGGTCACAGATGCGAGCTGATTCGGCACGCTCAGCCGGCGGCATA							2390
QY	121	GAAAGCGCTGCATTCACAGCGGCTGGCAGGCGGTAAACCGCTTGACAGGCGCATATGCGACG							180
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QY	181	GTCCGGCGGGGACGCCCGGAAACAGCATTCGGTTTACAGACCCGCGAGAAAGCGGTGCGCATC							240
Db	2329	GTCCGGCGCGGACGCCCGGAAACAGCATTCGGTTTAAAGGCGAGAAAGCGGTGCGCGCG							2270
QY	241	CGCGGATTCATATGGCCGACCGCGCACCGCGCGACG-----GGCGGACGGCGTCTGTCAG							294
Db	2269	CGCCCGGTGATTCGGTATGCGGATGCGCGGATGCGCGCGCGCGCGACGCGCGTTCGTCGGGCGGCGCC							2210
QY	295	GTCCGCGCCCGCGATGCGATCCGCGACTCTGCGCGCATATGGGACGCGATATCCGATGAC							354
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QY	355	GGGCTGGAACAGCCCTGCCCCCAACCCCAACCGGACAGCGCCCCCGCGTGTATGCGCGCA							414
Db	2149	CGGATGAAGAACCCCGCGCGCATCTCCAACGGGAAACAGCCCGCGCGGTATGCGCCCA							2090

QY	41.5	GAAGCGCTATGCGGTATGAGGCGCAGGCGCATATGGGACAGAAATGCCCCCTTTGGCCCGCATCTC	474
Db	2089	GAGGCCCGCCGCATATGAGGCGCAGGCGCATATGGAGATATGCCCTTTGGCCCGCATCTC	2030
QY	475	CTGCCCCGCTCGAGCCCGCGCTGGCGGCAATAGTCACGACGCGCTGGCGCAGCGCGCATC	534
Db	2029	GCCCCCGGTCAGAGCCCTGTGGCGGGCATATAGTCGTATGGAGACCGCGCGCATAGCGTCTC	1970
QY	535	GTTCAGATTCGCGCGCGCTGGCTGGTAGCGCGTATCCTCGATCAGAGATGCGGGTGGGACTGAA	594
Db	1969	GTCCAGATTCGCGCGCATATGAGAAATACGCGGTGTCTCGATCAGAGATGCGCGTTCGAGAGAA	1910
QY	595	GGGCGAGCATATGATGAAGACGGGTACCGGTCATCTGGCGGAAACGGTGGCGTCTCATATATAT	654
Db	1909	GGGCGAGCATATGATGAAGACGGGTACCGGTCGTCTGGGTGACAGGTGGGTCTCATATATAT	1850
QY	655	CGGGCGCTTCGACGCGCATATGGGGGCGCTCGGTCTCGATCTCGACGCGCCAAGAAATTTCTGGA	714
Db	1849	CGGGCGGGGGCAGCGCGTGGGGGCGGTGGGTCTCGATCTCGACACCCAAGAAATTTCTGGA	1790
QY	715	ACCCACGGTCAAGTGGGGGCTCTCGACGCGCACACGAGGCGTTCGATCAGCAGGACGCTC	774
Db	1789	ACCCACGGTCAAGTGGGGGCTCTCGACGCGCACACGAGGCGTTCGATCAGCAGGACGCTC	1730
QY	775	GATCCGCGAGCGCTGCTCCGTCATCGGTGGCGCGCGGTATCTGTCAGCGTTCGCGCATGCTATT	834
Db	1729	GATCCGCGGTGCGCGCAGAGCAGCGTTCGCCCTTCGCGCATCTCAGCAGGCGGATGTGCTGTC	1670
QY	835	CCACCGCAGATTCGACACCGCTTGACGAGC-----CCGATTCAGCGCGCGCGCTCGATCGA	888
Db	1669	CCAGCGGATCTTCGCGCGCGCGCGACCGGACCAACGCGATCGCGCAGCGCGCGCGCTTCAGCGA	1610
QY	889	GCCATAGCGCTGTCTGTCAGCGCGCGCGGATGCTCGGAGAAACGCGACTTCCTGATCCGTCGA	948
Db	1609	CCCGTACCGGTTAGCGCAGCGCGCGCGGAGAAAGCGCACCTCTGTCGCGGCA	1550
QY	949	TTCCGCGCGAGCAATGCGCGCAGCGCGCGCGCGCATTCCTGGCGGCAAAATCTCGTGTCTG	1008
Db	1549	GTTCGCGCGCGCGCAGGAGGCTTCAGCGCGCGCGCAGCGCATGTCGCGCAGCAGGTGGGGTCTGT	1490
QY	1009	GCAGGACAGGTTGCTGTCTGTCAGAGGCGCGGACCGCGCTCGAGCATCATGATGCGCGC	1068
Db	1489	GCAGGACAGGTTGCTGTCTGTCAGCGGTCTTGCGCATGTCACGACACACACAGCGGAG	1430
QY	1069	ATCCGCTCTGCGGTTCGCGAAGCGCGCATCGCGCACCGGACAGCGCGCGCGCGC	1128
Db	1429	GTCCGCGCGCGCGCGCGCGCGCGCGCATCGCGCGCGCGCGCGCGCGCGCGCGCGC	1370
QY	1129	GATCAGCATATGCTCTCA	1148
Db	1369	CAGCAGCAGTCATGCTCA	1350

RESULT 14

US-09-335-919-7/c

Sequence 7, Application US/09335919

Patent No. 6150130

GENERAL INFORMATION:

APPLICANT: MISAWA, No. 6150130iniko

APPLICANT: KONDO, Keiji

APPLICANT: KAJIWARA, Susumu

APPLICANT: YOKOYAMA, Akihito

TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF

TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,919
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5330
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2886 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-335-919-7

Query Match      55.8%; Score 640.8; DB 3; Length 2886;
Best Local Similarity 73.4%; Prid.No. 6.1e-122;
Matches 851; Conservative 0; Mismatches 297; Indels 12; Gaps 2

QY      1 TCATGCTCTCCCTGACAGAGGGGCGTTCCGGGACGAGCGCAAGCGCTGCGACAGCGG
DB.      2509 TCATGCGTTTTCCTTACAGAGGGAGCGTTCCGGGACGAGCGAGATGGCCGTGCCAAGGGG
QY      61 AATGGGCGGGGCGTCCGCTGATGCGATGCGAAGCGCGTCCGCAATGTCAGAGCGCCCGGCATTA
DB      2449 AATGGAGAGCTTGGCCGCTGACGATGCGGACGATGTCGCCCAAGCTCAAGCGGCGGCATTA
QY      121 GAAGCGCTCGATCAGCGGCTCGGACGAGCGGCTGAGACCGCTTGACAGCAGGCGATAGCGAGC
DB      2389 GAACGCTTCATGATGATCCATCGGCGATCGGCTAGAGACCGCTGACAGCAGGCTTAGCGCGG
QY      181 GTCCGGGCGGAGCGCGCGGAACAGATCCGCTTACAGCAGCCGCAAGAACGGTCCGCGATC
DB      2329 GTCCGGGCGGAGCGCGCGGAACAGATCCGCTTCAAAAGCGCAAAAGCGTCCGCGCG
QY      241 CGCGGATCATGATGGCCCAAGCGCGCAAGCGCGCAAGCGCGCAAGCGCGCGCGCGCGCGCG
DB      2269 CGCCCGGCTCATCGCGTAAATGCGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
QY      295 GTCCGCGCGCGCGCATGCGATCCGCGACCTTGCAGCGGCGATAGGCGCAAGATATCCGCTGAC
DB      2209 GAACAGACCCCGCACACAGTCCGCGCACTTGTGCGCATATAGGCGAATATAGCCGCTGAC
QY      355 GCGGTGGAACAGCCCTGCGCCCAAGCGCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCA
DB      2149 CGGATGAAAGAACCCCGCGCGCAAGTCCCAAGCGGAACAGGCGCGCGCGCGCGCGCGCGCA
QY      415 GAACCGTATGCGCTCATGAGGCGCAAGCGCGATGAGGCGAGATGCGCCCTTTTGCAGCGCGATGTC
DB      2089 GAAGCGCGCGCGCATCATATGAGCGCAAGCGCGATGAGGAAGATATGCGCGCTTGCAGCGCGCAAGCCTC
QY      475 CTGCGCGGTCAGCGCGCGCTTGGCGGCGATGATGCAGCGAGCGCTGCGCGCAAGCGCGCATC

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535 GTCCGATGCGCGCGCTGCTGAGCGGATCTCTGATCAGATGCGGGTGGAGCTGA 594
1969 GTCCGATGCGCGCGCTGAGTGAAGCGGTGCTGCTGATCAGATGCGGGTGGAGAG 1910
595 GGGCAGCAGATGATGAGGCGGTACCGCTGCTGAGCGGATGCGGTGCGCTCAGTAT 654
1909 GGGCAGCAGATGATGAGGCGGTACCGCTGCTGAGCGGATGCGGTGCGCTCAGTAT 1850
655 CGGGCGCTGACCGCATGAGGCGGCGCTGCTGCTGATCTGACCGCCAGCAATTTCTGAA 714
1849 CGGGCGGGGACGCGGTGAGGCGGCGCTGCTGATCTGACACCAATTTCTGAA 1790
715 ACCGAGCGTGAAGTGGGGGTCTGACAGCGGACCAAGGGGTGATGACAGCAGGAGCTC 774
1789 ACCGAGCGTGAAGTGGGGGTCTGACAGCGGACCAAGGGGTGATGACAGGAGCTC 1730
775 GATCCGCGAGCGCTGCTGAGCGGTGCGCGCGGTATGTCAGCGGTGCGAGATGAGTAT 834
1729 GATCCGCGGTGCGCGAGGACAGGTGCGCGCGGTGCTGAGCGGTGCGAGATGAGTAT 1670
835 CCACCGCAGATGACACCTCTGACAGC-----CGATCAGCGCGCGCTGCTGATGCA 888
1669 CCAGCGGATCTCGCGCGCGCGAGCAGCAGCGCATCCGCGCGCGCGCTGCAAGCGA 1610
889 GCGATAGCGCTGCTGACAGCGCGCGCGGAAATGTCGAGGAAAGCGGATCTCTGATCTGCA 948
1609 CCGTGAACCGGTGCGCGCGCGCGCGGATGCGGAGGAAAGCGGATCTCTGATCTGCA 1550
949 TTGCGCGCAGCAATGAGGCGAGAGCGCGCGCGCATTTGCGGCGGAAAGTCCGTGCTG 1008
1549 GTTGGCGCGCGCGCGAGGCGCTTCAAGCGCGCGCGCGCATGCGGAGAGTCCGGGTGCTG 1490
1009 GCAAGCAGAGTGTGCTGCTGCGAGGCGCGCGCGCATGCGGAGATGATGATGCGCGCG 1068
1489 GCAGAGCAGAGTGTGCTGCTGAGCGGTCTGCGGAGATGATGATGAGAGAGCGCGCAG 1430
1069 ATCCGCTGCGGCGTGGAGAGCGGAGCGGATGAGCGGAGCGGAGCGCGCGCGCGCG 1128
1429 GTTGGCGCGCGCGCGCGCGCGCGCGGAGCGGAGCGGATGAGCGGAGCGCGCGCGCG 1370
Gy - 1129 GATCAGCAGATGATGCTCA 1148
Db 1369 CAGCAGCAGTATGCTCA 1350

RESULT 15
US-08-095-726-13/c
Sequence 13, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095, 726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785, 566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-095-726-13

Query Match 17.4%; Score 200; DB 1; Length 1235;
Best Local Similarity 50.8%; Pred. No. 5e-32;
Matches 563; Conservative 0; Mismatches 530; Indels 15; Gaps 3;

45 CGGCTGCGAGAGCGGATGAGCGCGCTGCGGTGACGATGCGAAGCGCGTCCGCAATG 104
Db 1130 CAGACTTGGCCAGCGGAAACCGGTGCTTCCCTGTAATAATCGCGCTTATCAAGAG 1071
Gy 105 TCAGGCGCGCGCATGAGAGCGCTTGATCAGCGCTGCGGAGCGGATGAGAGCGCTGCA 164
Db 1070 AGAGCGCAGCGCGGATGAGAGCGCTCTACGTTGGGCTCGGAGCGCCATGAAAGCGCTCA 1011
Gy 155 GCAGCGCATGAGCAGCGTGGCGCGCGCGCGGAGAGAGATCCGTTGACAGCGCGCA 224
Db 1010 TCACCGCGCAGCGGTTCTCTCGCGCGCGCGCGGAGAGAGATCCGTTGACAGCGCGCA 951
Gy 225 GGAAGC---GGTGGCATCCGCGCGCATGAGCGCGCGCGCGCGCGCGCGCGCGCG 281
Db 950 AGAATCCCTGCTGCG 891
Gy 282 ACGCGGTGTAAGTTCG 341
Db 890 CGCTGCCAGCG 831
Gy 342 AATATCCGTGACGCGGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 401
Db 830 AATAGCCAGGTGATGAGGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 771
Gy 402 CGTGTGCGCGCAGAGCGCTATGCGGTATGAGCGCGCGCGCGCGCGCGCGCGCGCG 461
Db 770 TGGGCCACAGAGCGCTGATGATGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 714
Gy 462 CGCGCGCATCTCTGCG 521
Db 713 CGCGTTCAAGCTGGCG 654
Gy 522 CAGCGCGCGCATCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 581
Db 653 GTAGGCGATTTATCATCAAGCGCTGCGGAGATTTGCGGCGCGCGCGCGCGCGCG 594
Gy 582 GGGTGGAGCTGAGGCGCAGAGATGATGAGAGCGGTACCGCTCATCTGCGGAGCGTGC 641
Db 593 TGTGCGCGGAGAGCG 534
Gy 642 CGTTCATGATCATGCGGCGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 701
Db 533 CATCATCAGATCGGTACGCGTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 474
Gy 702 CGAATTTCTGAGAAACCAAGCGTCAAGTGGCGGTCTGACAGCGCGCGCGCGCGCG 761
Db 473 GAAAGAGCTGATAGCGGCTTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 414

```
QY 762 CGCAGGCGCCTCGATCCGAGACCGTCCGTCAGCGTCCGCGGATATCGTCCAGCGTCG 821
Db 413 CCGCTCCGCGACAGCAGCGCCTCACCGTTGGCAAGCGCAGCTATTGGGTAACACTCCG 354
QY 822 CGCATGCGTATTCCACCGCAGATCGACCC-----TGCAGACGCCGATCAGCG 872
Db 353 TCACCGAACAGTTTACGAGATGTCTCCCCAGCGCCTGATGCAAGGCTCGGCAAGC 294
QY 873 CGCCCGCTCGATCGAGCCATAGCCTGTGTCAAGCGCGCGCAATGTGTGGGAAACCGCA 932
Db 293 GCTGTAGGTAAATGAGTAGTAGCCGCGCGAGCGACGCGCAGATCGGGAACCTGCA 234
QY 933 CCTCTGATCCGTCATTCGCGCGCGAGCAATGGGCGCAGCGCGCAGCCATTGGGGCG 992
Db 233 CCTCATAGCCCGGCGAGCGGTGGCCACAGCGGGGCGACCGCGGTGTGCCCCGGGAG 174
QY 993 AAGATCCGTGTGTGTCAGAGCAGAGTGTGTGTCCAGGGGCGCGACCGCGCTCGA 1052
Db 173 TCAGATCGTCTTCATGGAATGACCAAGTATGTTCCCGCGGCTGTCTCCCGGCTCGA 114
QY 1053 GCATCAAGATGCGCGCATCCGCTCTGGGGTCCGAAAGCGAGCGGATCAGCGCACCG 1112
Db 113 TCAGCAGCAGGTAAAGCTGCGGGTAGCGCTGCGCAGACGCCAGGATCAGCCCGTTGG 54
QY 1113 ACAGCCCCCGCGCCGCGATCAGCAGATC 1140
Db 53 CAGGCGCGCGCCGACTAAATCAGATC 26
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Search completed: June 22, 2005, 01:09:49
Job time : 312.581 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2005, 15:45:26 ; Search time 751.928 Seconds
(without alignments)
9045.769 Million cell updates/sec

Title: US-10-695-980-1_COPY_5794_6942

Perfect score: 1149

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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 295987067 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003as:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	8625	2 AAT45143	Aat45143 Flavobact
2	1149	100.0	8625	2 AAV40146	Aav40146 Flavobact
3	1147.4	99.9	11233	2 AAV40151	Aav40151 DNA sequ
4	640.8	55.8	1161	2 AAG99489	Aag99489 3 hydroxy
5	640.8	55.8	1161	2 AAV84076	Aav84076 Carotenol
6	395.4	34.4	1966	11 Aax19116	Aax19116 Agrobacte
7	394	34.3	1944	11 ADQ96933	Adq96933 CrtrCrtY
8	236.4	20.6	1185	10 ADQ96933	Adq96933 CrtrCrtY
9	236.4	20.6	1185	10 ADQ96933	Adq96933 CrtrCrtY
10	213.4	18.3	12753	12 ADM98599	Adm98599 Bradyrhiz
11	209.8	18.3	1149	6 AAD35511	Aad35511 Geranylge
12	209.8	18.3	1149	8 AAT14191	Aat14191 Pantoea s
13	209.8	18.3	1149	8 ACC44761	Acc44761 Pantoea s
14	209.8	18.3	1149	12 ADQ14628	Adq14628 Pantoea s
15	209.8	18.3	1149	12 ADQ14628	Adq14628 Pantoea s
16	209.8	18.3	1149	12 ADQ48638	Adq48638 Pantoea s
17	209.8	18.3	1149	12 ADQ94455	Adq94455 Crty codi
18	209.8	18.3	8609	12 ADQ14666	Adq14666 Reporter
19	209.8	18.3	8609	12 ADQ26394	Adq26394 Carotenoi
20	209.8	18.3	8609	12 ADQ77262	Adq77262 Nucleotid

C 21	209.8	18.3	8609	12	ADQ48673	Adq48673 Plasmid p
C 22	209.8	18.3	8609	12	ADQ94478	Adq94478 Plasmid p
C 23	200	17.4	1235	2	AAT40795	Aat40795 Lycopen
C 24	200	17.4	1235	2	AAT91547	Aat91547 Brwinia h
C 25	198.4	17.3	1234	2	AAQ13722	Aaq13722 Lycopen
C 26	198.4	17.3	1234	2	AAQ13723	Aaq13723 Lycopen
C 27	198.4	17.3	1235	2	AAT40796	Aat40796 Recombina
C 28	198.4	17.3	1235	2	AAT91548	Aat91548 Genetica
C 29	174.8	15.2	1149	2	AAQ06295	Aaq06295 Sequence
C 30	174.8	15.2	1149	2	AAV84083	Aav84083 Carotenoi
C 31	174.8	15.2	1149	2	AAQ19120	Aaq19120 Brwinia u
C 32	174.8	15.2	6424	12	ADP74122	Adp74122 Pantoea a
C 33	174.8	15.2	6918	2	AAQ06299	Aaq06299 Sequence
C 34	174.8	15.2	7494	8	ABZ69177	Abz69177 Vector co
C 35	174.8	15.2	8547	8	ABZ69178	Abz69178 Vector co
C 36	150.8	13.1	1167	2	AAV73182	Aav73182 C. utrilis
C 37	138.8	12.1	1631	12	ADQ61158	Adq61158 Alcaligen
C 38	138.8	12.1	1631	12	ADQ61075	Adq61075 Alcaligen
C 39	138.8	12.1	1631	13	ADQ38244	Adq38244 Alcaligen
C 40	138.8	12.1	1631	13	ADQ03859	Adq03859 Alcaligen
C 41	138.8	12.1	1631	13	ADQ03939	Adq03939 Alcaligen
C 42	99.6	8.7	1176	10	ACF70994	Act70994 Photorhab
C 43	99.6	8.7	110000	10	ACF67367	Act67367 Photorhab
C 44	99.6	8.7	110000	10	ACF65388	Act65388 Photorhab
C 45	99.6	8.7	110000	10	ACF65388_07	Act65388_07 Photorhab

ALIGNMENTS

RESULT 1	
ID AAT45143	standard; DNA; 8625 BP.
XX AAT45143;	
AC	
XX	
DT 17-OCT-2003	(revised)
DT 08-MAR-1997	(first entry)
XX	
DB Flavobacterium carotenoid biosynthesis cluster DNA.	
XX	
KW Carotenoid; lycopen; beta-carotene; echinenone; canthaxanthin;	
KW zeaxanthin; adonixanthin; astaxanthin; crtE;	
KW geranylgeranyl pyrophosphate synthase; GGPP synthase; crtB;	
KW prephytylene synthase; phytylene synthase; crtI; phytylene desaturase; crtY;	
KW lycopen cyclase; crtZ; beta-carotene hydroxylase; ds.	
XX	
OS Flavobacterium sp. ATCC 21588; WT (ATCC 21588).	
XX	
FH	
FT	
Key	location/Qualifiers
CDS	2..1168
FT	/*tag= a
FT	/label= ORF-5
FT	1180..2355
CDS	/*tag= b
FT	/label= ORF-1
FT	2521..3408
CDS	/*tag= c
FT	/label= crtE
FT	/product= "GGPP synthase"
CDS	complement(3405..4316)
FT	/*tag= d
FT	/label= crtB
FT	/product= "(pre)phytylene synthase"
CDS	complement(4313..5797)
FT	/*tag= e
FT	/label= crtI
FT	/product= "phytylene desaturase"
CDS	complement(5794..6942)
FT	/*tag= f
FT	/label= crtY
FT	/product= "lycopen cyclase"
CDS	complement(6939..7448)

FT	/tag= g
FT	/label= CRYZ
FT	/product= "beta-carotene hydroxylase"
FT	complement(7767. .8315)
FT	/tag= h
FT	/label= ORF-16
FT	misc_difference 8348. .8349
FT	/tag= i
FT	/note= "bases 8348-8349 are given as mn in the specification"
FT	misc_difference 8539. .8540
FT	/tag= j
FT	/note= "bases 8539-8540 are given as mn in the specification"
FT	misc_difference 8581
FT	/tag= k
FT	/note= "base 8581 is given as n in the specification"
FT	misc_difference 8590
FT	/tag= l
FT	/note= "base 8590 is given as n in the specification"
FT	misc_difference 8592
FT	/tag= m
FT	/note= "base 8592 is given as n in the specification"
FT	misc_difference 8602. .8604
FT	/tag= n
FT	/note= "bases 8602-8604 are given as nn in the specification"
FN	
PN	EP747483-A2.
PD	11-DEC-1996.
PP	29-MAY-1996; 96EP-00108556.
PR	09-JUN-1995; 95EP-00108888.
PR	(HOFF) HOFFMANN LA ROCHE & CO AG F.
PA	Hohmann H, Pasamontes L, Tessier M, Van Loon A;
XX	WP1; 1997-023160/03.
DR	P-PSDBI, AAM06513, AAM06514, AAM06515, AAM06516, AAM00871, AAM06517,
DR	AAM06518, AAM06519.
XX	Flavobacterium gene sequences encoding carotenoid biosynthesis enzymes -
PT	for the production of carotenoid(s), useful in foods and animal feeds.
XX	Example 2; Fig 7; 80pp; English.
PS	
XX	
CC	Genomic DNA (AAT4514) of Flavobacterium sp. R1534 includes genes of the
CC	carotenoid biosynthesis pathway. The sequence was deduced from inserts of
CC	6 clones obtd. from genomic libraries e.g. by PCR amplification (see also
CC	AAT4514-45) and use of partial clones to screen the library. The
CC	identities of the gene products (see also AAM06513-19 and AAM00871) were
CC	deterd. by examining carotenoid accumulation in E. coli hosts transformed
CC	with deleted variants of the gene cluster. The isolated genes can be used
CC	in different combinations to produce carotenoids in transformed host
CC	cells. (Updated on 17-OCT-2003 to standardise OS field)
XX	
XQ	Sequence 8625 BP; 1458 A; 2898 C; 2964 G; 1295 T; 0 U; 10 Other;

Query Match	100.0%	Score 1149;	DB 2;	Length 8625;
Best Local Similarity	100.0%	Pred. No. 1.3e+206;		
Matches 1149; Conservative	0;	Mismatches	0;	Gaps 0

QY	Db	QY	Db
1	5794	61	5854
TCATCTCTCTCTCTCAGACAGGGGGCGTTCCGGGACAGCCACAGGCTTGGCAACAGGG	TCATCTCTCTCTCTCAGACAGGGGGCGTTCCGGGACAGCCACAGGCTTGGCAACAGGG	AATGGGCGGGCGCTCCGGTGACGATGCGAAGCCGGTTCGGCCAAATGTTCAGGCGCCCGGCATTA	AATGGGCGGGCGCTCCGGTGACGATGCGAAGCCGGTTCGGCCAAATGTTCAGGCGCCCGGCATTA
60	5855	120	5913

QY	121	GAAGGCTCTCATTCAGCGGCTGCGGAGCGGATGAAACGGCTGACGACGGCATATACGACG	180
Db	5914	GAAGGCTCTCATTCAGCGGCTGCGGAGCGGATGAAACGGCTGACGACGGCATATACGACG	5977
QY	181	GTCCGGCGGGCAAGCCCGGAAACAGCATCCGTTTCAGCAGCCGACGAAAGCGGTCCGATC	240
Db	5974	GTCCGGCGGGCAAGCCCGGAAACAGCATCCGTTTCAGCAGCCGACGAAAGCGGTCCGATC	6033
QY	241	CGCCGATTCGATTCAGCCGCGCACCGCGGACGAGGCGGACCGGATCGTACGGTCGCG	300
Db	6034	CGCCGATTCGATTCAGCCGCGCACCGCGGACGAGGCGGACCGGATCGTACGGTCGCG	6093
QY	301	CGCCGCGATTCGATTCAGCCGCGCACCGCGGACGAGGCGGACCGGATTCGATTCGCG	360
Db	6094	CGCCGCGATTCGATTCAGCCGCGCACCGCGGACGAGGCGGACCGGATTCGATTCGCG	6153
QY	361	GAACAGCCCTTGCCCGACCCCAACCGGACACCGCCCCCTTCGCGTTCGGTGGCCGACAGCC	420
Db	6154	GAACAGCCCTTGCCCGACCCCAACCGGACACCGCCCCCTTCGCGTTCGGTGGCCGACAGCC	6211
QY	421	TATGCGCTCATTCGAGGCGCAGCGCATGGGAGAGATGCCCTTTTCGCGCCGATTCCTGCGC	480
Db	6214	TATGCGCTCATTCGAGGCGCAGCGCATGGGAGAGATGCCCTTTTCGCGCCGATTCCTGCGC	6277
QY	481	GCTCCAGCCCGCGCTTGCGGCGCATTCAGCGACGCTTCGCGCAGCGCGCCATTCGTCAG	540
Db	6274	GCTCCAGCCCGCGCTTGCGGCGCATTCAGCGACGCTTCGCGCGCAGCGCGCCATTCGTCAG	6333
QY	541	ATCCCGCGCGCTTCGCTGTACCGCGTATTCCTCGATTCAGGATTCGGGGGCTGAAAGGCGACG	600
Db	6334	ATCCCGCGCGCTTCGCTGTACCGCGTATTCCTCGATTCAGGATTCGGGGGCTGAAAGGCGACG	6397
QY	601	CAGATAGATGAAAGCGGTACCCGTCATTCGCGGAAACGGTCGCGTCATTCATTCAGGCGG	660
Db	6394	CAGATAGATGAAAGCGGTACCCGTCATTCGCGGAAACGGTCGCGTCATTCATTCAGGCGG	6453
QY	661	CTCGACGCCATTCGGGGGGGCTCGGTCTCGATCTTCAGCGCCCAAGATTTCTGAAACCCAC	720
Db	6454	CTCGACGCCATTCGGGGGGGCTCGGTCTCGATCTTCAGCGCCCAAGATTTCTGAAACCCAC	6511
QY	721	GGTCCAGTTCGGGGGCTTCGACGAGCACACAGGGCGTCGATTCAGCAGCAGGACCTTCGATCG	780
Db	6514	GGTCCAGTTCGGGGGCTTCGACGAGCACACAGGGCGTCGATTCAGCAGCAGGACCTTCGATCG	6577
QY	781	CGAGCGCTCCGTCAGCGCTCGCGCGGTATTCGTCAGCGGTGCGCATGCGTATTCACCG	840
Db	6574	CGAGCGCTCCGTCAGCGCTCGCGCGGTATTCGTCAGCGGTGCGCATGCGTATTCACCG	6633
QY	841	CAGATTCGACACCTTCGACAGCCCGCATTCAGCGCGCGCCCTTCGATTCAGGCCATTAACGCT	900
Db	6634	CAGATTCGACACCTTCGACAGCCCGCATTCAGCGCGCGCCCTTCGATTCAGGCCATTAACGCT	6697
QY	901	CGTCAGGCGGCGCGAATGCTCGGAGAAACGCGACTTCGATTCGCTCATTTCCGCCCGACG	960
Db	6694	CGTCAGGCGGCGCGAATGCTCGGAGAAACGCGACTTCGATTCGCTCATTTCCGCCCGACG	6753
QY	961	AATGGGCGACAGGCGCGCGCATTCGAGCGAAAGATTCGTTGTTGGCAGGACCAAGGT	1021
Db	6754	AATGGGCGACAGGCGCGCGCATTCGAGCGAAAGATTCGTTGTTGGCAGGACCAAGGT	6811
QY	1021	GTGCTGCTCCGAGGGGGCGGACCGGCGGTCGAGCATTCAGATTCGCGCATTCGCGGCTCGG	1081
Db	6814	GTGCTGCTCCGAGGGGGCGGACCGGCGGTCGAGCATTCAGATTCGCGCATTCGCGGCTCGG	6877
QY	1081	GTTCGGAACGGCAACGGGATTCAGCGCACCGGACAGCCCGCGCCCGCGATTCAGCAGATC	1144
Db	6874	GTTCGGAACGGCAACGGGATTCAGCGCACCGGACAGCCCGCGCCCGCGATTCAGCAGATC	6933
QY	1141	ATGGCTCAT 1149	
Db	6934	ATGGCTCAT 6942	

Db	6874	GTCTGGAAAGGGAACGGCGATCAGGCAACGGACAGCCCGCGCCCGCGATCAGCAGATC	6933
Qy	1141	ATGGCTCAT	1149
Db	6934	ATGGCTCAT	6942

XX	AAV40146; standard; DNA; 8625 BP.
XX	AAV40146;
AC	
XX	
XX	
DT	10-AUG--1999 (first entry)
XX	
DE	Flavobacterium sp. R1534 nucleotide sequence.
XX	
KM	Carotenoid pigment; canthaxanthin; R1534; crtB; prephytyene synthase;
KM	crtI; phytoene desaturase; crtX; lycopen cyclase; GGP synthase; crtE;
KM	crtK2356; beta-carotene beta-oxygenase; food product; fermentation; ds.
OS	
XX	Flavobacterium sp.
PN	JPI1055497-A.
PD	16-JUN-1998.
XX	
PF	02-DEC-1997; 97JP-00348653.
XX	
PR	02-DEC-1996; 96EP-00810839.
XX	
PA	(HOEF) HOFPMANN LA ROCHE & CO AG F.
DR	WPI; 1998-391048/34.
XX	P-PDSB; AAW69530, AAW69531, AAW69532, AAW69533, AAW69534.
PT	Preparation of carotenoid - comprises fermentation with transformed cell.
XX	
PS	Claim 1; Fig 7-21; 80pp; Japanese.
CC	The invention describes the preparation of carotenoid pigments e.g.
CC	canthaxanthins using a cell transformed by a vector having DNA sequences
CC	(a) to (e) or substantially homologous sequences. (a) a DNA sequence
CC	(crtE) coding GGP synthase of Flavobacterium sp. R1534; (d) a DNA
CC	sequence (crtB) coding prephytyene synthase of Flavobacterium sp. R1534;
CC	(c) a DNA sequence (crtI) coding phytoene desaturase of Flavobacterium
CC	sp. R1534; (d) a DNA sequence (crtY) coding lycopene cyclase of
CC	Flavobacterium sp. R1534, and (e) a DNA sequence (crtK2356) coding beta-
CC	carotene beta-oxygenase of a microbe E-396 (FERM BF-4283). The carotenoid
CC	or a carotenoid mixture can also be used in preparation of food products.
CC	The method is an improved method of fermentation for carotenoid
XX	production
SQ	Sequence 8625 BP; 1458 A; 2898 C; 2964 G; 1295 T; 0 U; 10 Other;
	Query Match 100.0%; Score 1149; DB 2; Length 8625;
	Best Local Similarity 100.0%; Pred. No. 1,36-206;
	Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 TCATGCTCTTCCTCAGAGGGGGCGTTCCGGGCAGGAGCGGCTGTGCAAGCGG 60
DB	5794 TCATGCTCTCTCTCAGAGGGGGCGTTCGGGCAGGAGCGGCTGTGCAAGCGG 5855
OY	61 AATGGGCGGGCGTCCGGTGACGATCCGAAGCCGGTCCGCAATGTTCAGCGGCCGCGCATTA 120
DB	5854 AATGGGCGGGCGTCCGGTGACGATCCGAAGCCGGTCCGCAATGTTCAGCGGCCGCGCATTA 5913
OY	121 GAAGCGCTCGATCAGCGGCTGGCGGAGCGGTAGAACCGCTTCAGCAGGCGATAGCGAGC 180
DB	5914 GAAGCGCTCGATCAGCGGCTGGCGGAGCGGTAGAACCGCTTCAGCAGGCGATAGCGAGC 5973
OY	181 GTCCGGGGCGGCGAGCGCGGAAGAAGATCCGTTTCAGAGCGGCGAAGAAAGCGGTCCGATTC 240
DB	5974 GTCCGGGGCGGCGAGCGCGGAAGAAGATCCGTTTCAGAGCGGCGAAGAAAGCGGTCCGATTC 6033
OY	241 CGCGCGATCGATGAGCCCAAGCCCGCACCGCGCGAGCGGGCGAGCGGGTGTTCAGAGTCCGCG 300
DB	6034 CGCGCGATCGATGAGCCCAAGCCCGCACCGCGCGAGCGGGCGAGCGGGTGTTCAGAGTCCGCG 6099
OY	301 CGCGCGATGAGCCCAAGCCCGCACCGCGCGATAGGGCGAGCGAATAATCCGGTTCAGCGGGTTC 360

Accession	Sequence	Position
Db	CGCCGCGATGGCATTCGGGACCTTCGGGGCATAGGGGACGCAATATCCGGTGAAGGGGTG	6153
6094	CGCCGCGATGGCATTCGGGACCTTCGGGGCATAGGGGACGCAATATCCGGTGAAGGGGTG	6153
Qy	GAACAGCCCTGACCCCAAGCCCAACCGGCAACCGCCCTTCGGGGTGTGCGCCAGAAAGCC	420
Db	GAACAGCCCTGACCCCAAGCCCAACCGGCAACCGCCCTTCGGGGTGTGCGCCAGAAAGCC	6213
Qy	TATGGCGTCATGGGCGCAGCGCGATGGGCGAGATGCCCTTTTCGGCGCGCATCTCTGCCC	480
Db	TATGGCGTCATGGGCGCAGCGCGATGGGCGAGATGCCCTTTTCGGCGCGCATCTCTGCCC	6273
Qy	GGTCAGGCCCCCGCTGGGCGGACATAGTCAGGAGACGCGCGCGCAGCGCGCCATCGTCAG	540
Db	GGTCAGGCCCCCGCTGGGCGGATAGTCAGGAGACGCGCGCGCAGCGCGCCATCGTCAG	6333
Qy	ATCCCGCCCGTCGCTGTAGCGCGGTATCTTCGATCAGATGCGGGTGGACTGAAGGGCAG	600
Db	ATCCCGCCCGTCGCTGTAGCGCGGTATCTTCGATCAGATGCGGGTGGACTGAAGGGCAG	6334
Qy	CAGATAGATGAAGCGGATACCGGTCACTCGCGGAAACGGTCGCTCATGATCATCGGGCG	6453
Db	CAGATAGATGAAGCGGATACCGGTCACTCGCGGAAACGGTCGCTCATGATCATCGGGCG	6394
Qy	CTGCACGCGAATGGGGGGGCTCGGTCTGATCTCGACGCCACGAATTTCTGGAAACCCAC	720
Db	CTGCACGCGAATGGGGGGGCTCGGTCTGATCTCGACGCCACGAATTTCTGGAAACCCAC	6454
Qy	GGTCAAGGTGCGGGGTCTCGACGCGCACACGCGGCTCGATCACGCGAGCGCTCGATCCG	780
Db	GGTCAAGGTGCGGGGTCTCGACGCGCACACGCGGCTCGATCACGCGAGCGCTCGATCCG	6514
Qy	CGAGCCGTCGCTCAAGCGTCGCGCGGTATGTCACGCGTCGCGCATATGCTATTCACCG	840
Db	CGAGCCGTCGCTCAAGCGTCGCGCGGTATGTCACGCGTCGCGCATATGCTATTCACCG	6574
Qy	CAGATTCACACCTCGACAGCGCCGATCAAGCGCGCGCGCGCTCGATCGAGGCGATAGCCGT	900
Db	CAGATTCACACCTCGACAGCGCCGATCAAGCGCGCGCGCGCTCGATCGAGGCGATAGCCGT	6634
Qy	CGTACAGCGCGCGCAATATGTCGGGAAACGCACTCTCGATCCGTCATTTCGCGCGACG	960
Db	CGTACAGCGCGCGCAATATGTCGGGAAACGCACTCTCGATCCGTCATTTCGCGCGACG	6694
Qy	AATGAGCGACAGCGCGCGCACCATTCGGGGGAAAGATCCGTGTCTGTGGCAGACAGGT	1020
Db	AATGAGCGACAGCGCGCGCACCATTCGGGGGAAAGATCCGTGTCTGTGTGGCAGACAGGT	6754
Qy	GTGCTGTGTCCGAGGGGGCCGACCGCGGTTCGAGATCAACGATGGGCGCATTCGGGTCTGGC	1080
Db	GTGCTGTGTCCGAGGGGGCCGACCGCGGTTCGAGATCAACGATGGGCGCATTCGGGTCTGGC	6814
Qy	GTCCGGAAGCGCAAGCGCGATCAGCGCACGCGCAGCGCGCGCGCGCGCGATCAGCAATC	1140
Db	GTCCGGAAGCGCAAGCGCGATCAGCGCACGCGCAGCGCGCGCGCGCGCGATCAGCAATC	6874
Qy	ATGGCTCAT 1149	
Db	ATGGCTCAT 6942	
RESULT 3		
AAV40151	standard; DNA; 11233 BP.	
AAV40151		
AAV40151		
10-AUG-1999	(first entry)	
DNA	sequence of plasmid pZea4.	
Carotenoid; pigment; canthaxanthin; R134; crtB; prephytyene synthase;		
crtII; phytyene desaturase; crtY; lycopene cyclase; crtW396; pZea4;		
beta-carotene beta-oxygenase; food product; fermentation; ds.		

XX Synthetic.
OS JP10155497-A.
PN 16-JUN-1998.
XX 02-DEC-1997; 97JP-00348653.
XX 02-DEC-1996; 96EP-00810839.
XX (HOPF) HOFFMANN LA ROCHE & CO AG F.
XX WPI; 1998-391048/34.
XX Preparation of carotenoid - comprises fermentation with transformed cell.
XX Example 2; Fig 42-53; 80pp; Japanese.
XX The invention describes the preparation of carotenoid pigments e.g.
XX canthaxanthine using a cell transformed by a vector having DNA sequences
XX (a) to (e) or substantially homologous sequences. (a) a DNA sequence
XX (crtE) coding GSP synthase of Flavobacterium sp. R1534; (b) a DNA
XX sequence (crtB) coding prephytyene synthase of Flavobacterium sp. R1534;
XX (c) a DNA sequence (crtI) coding phytyene desaturase of Flavobacterium
XX sp. R1534; (d) a DNA sequence (crtY) coding lycopenase of
XX Flavobacterium sp. R1534; and (e) a DNA sequence (crtN2396) coding beta-
XX carotene beta-oxygenase of a microbe E-396 (FERM BP-4283). The carotenoid
XX or a carotenoid mixture can also be used in preparation of food products.
XX The method is an improved method of fermentation for carotenoid
XX production
SQ Sequence 1123 BP; 2142 A; 3525 C; 3605 G; 1960 T; 0 U; 1 Other;

Query Match 99.9%; Score 1147.4; DB 2; Length 11233;
Best Local Similarity 99.9%; Pred. No. 2.6e-206;
Matches 1148; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATGCTCTCTCTGAGAGAGGGGGGCTTCGGGACAGGCGACCGGCTTCGACAGCGG 60
DB 6476 TCATGCTCTCTCTCTGAGAGAGGGGGGCTTCGGGACAGGCGACCGGCTTCGACAGCGG 6535
QY 61 AATGGGCGGGCGTCCGGTACGATGCGAAGCCGGTCCGCAATGTCAGGCGCCCGCAT 120
DB 6536 AATGGGCGGGCGTCCGGTACGATGCGAAGCCGGTCCGCAATGTCAGGCGCCCGCAT 6595
QY 121 GAAGCGCTGATCAGCGGCTGCGGACGGCGGTAAGAACCGCTGACAGAGCGATAGGACG 180
DB 6596 GAAGCGCTGATCAGCGGCTGCGGACGGCGGTAAGAACCGCTGACAGAGCGATAGGACG 6655
QY 181 GTCCGGCGGGACCGCGGAACGATCGGTTCAAGCAGCCGACAGGAACGGATCGGATC 240
DB 6656 GTCCGGCGGGACCGCGGAACGATCGGTTCAAGCAGCCGACAGGAACGGATCGGATC 6715
QY 241 CGCGGATGATGCGCCAGCCCGGACCGCGGACCGCGGACCGCGGACCGCGGATCGGATC 300
DB 6716 CGCGGATGATGCGCCAGCCCGGACCGCGGACCGCGGACCGCGGATCGGATC 6775
QY 301 CGCGGATGATGCGCCAGCCCGGACCGCGGACCGCGGACCGCGGATCGGATC 360
DB 6776 CGCGGATGATGCGCCAGCCCGGACCGCGGACCGCGGATCGGATC 6835
QY 361 GAACAGCCCTGCGCCCGGACCGCGGACCGCGGACCGCGGATCGGATC 420
DB 6836 GAACAGCCCTGCGCCCGGACCGCGGACCGCGGATCGGATC 6895
QY 421 TATGGCGTATGCGGCGGACCGGATGCGGACCGGATGCGGACCGGATCGGATC 480
DB 6896 TATGGCGTATGCGGCGGACCGGATGCGGACCGGATGCGGACCGGATCGGATC 6955
QY 481 GGTCCAGCCCGCTGCGGCGGATGTCAGCGAGCGCTTCGCGGACCGGATCGGATC 540
DB 6956 GGTCCAGCCCGCTGCGGCGGATGTCAGCGAGCGCTTCGCGGACCGGATCGGATC 7015

QY 541 ATCCGCCGCGTCTGCTAGCCGCTATCTTCATCAGATGCGGCGTGGACTGAAGGCGAG 600
DB 7016 ATCCGCCGCGTCTGCTAGCCGCTATCTTCATCAGATGCGGCGTGGACTGAAGGCGAG 7075
QY 601 CAGATGATGAAGCGGTAACCGGCTCATCTTCGGAACCGGTCGCTCATGATCATCGGCG 660
DB 7076 CAGATGATGAAGCGGTAACCGGCTCATCTTCGGAACCGGTCGCTCATGATCATCGGCG 7135
QY 661 CTCGACGCGATGCGGCGGCGTCTGATCTCGACGCGCGCAAGATTCTGGAACCGAC 720
DB 7136 CTCGACGCGATGCGGCGGCGTCTGATCTCGACGCGCGCAAGATTCTGGAACCGAC 7195
QY 721 GGTTCAGTGGCGGCTCTCGACGCGCGCAACCGGCGCTGATCAGCAGCGCGCTCATCG 780
DB 7196 GGTTCAGTGGCGGCTCTCGACGCGCGCAACCGGCGCTGATCAGCAGCGCGCTCATCG 7255
QY 781 CGAGCCGTCCTGACGCTCGCGCGGATTCCTTCAGCGCTCGGACATCGTATTCACCG 840
DB 7256 CGAGCCGTCCTGACGCTCGCGCGGATTCCTTCAGCGCTCGGACATCGTATTCACCG 7315
QY 841 CAGATCGACCGCTGACGCGCGGATTCCTTCAGCGCGCGGATTCCTTCAGCGCGGATTC 900
DB 7316 CAGATCGACCGCTGACGCGCGGATTCCTTCAGCGCGCGGATTCCTTCAGCGCGGATTC 7375
QY 901 CGTCAAGCGGCGGATGCTGCGGGAACGCGACCTCTGATCCGTCATTGCGCGCGACG 960
DB 7376 CGTCAAGCGGCGGATGCTGCGGGAACGCGACCTCTGATCCGTCATTGCGCGCGACG 7435
QY 961 AATGGCGCAACAGCGCGCGGATTCGCGGGAAGATCCGTCGTCGTCGACGACAGT 1020
DB 7436 AATGGCGCAACAGCGCGCGGATTCGCGGGAAGATCCGTCGTCGTCGACGACAGT 7495
QY 1021 GTGCTGCTCCAGCGGCGCGGACCGCGGCTGACGATCGATGCGGATCGGCTGCG 1080
DB 7496 GTGCTGCTCCAGCGGCGCGGACCGCGGCTGACGATCGATGCGGATCGGCTGCG 7555
QY 1081 GTGCGAAGCGGACCGGATTCAGCGGACCGGACCGCGCGCGGATTCAGCGATC 1140
DB 7556 GTGCGAAGCGGACCGGATTCAGCGGACCGGACCGCGCGGATTCAGCGATC 7615
QY 1141 ATGCTCAT 1149
DB 7616 ATGCTCAT 7624
RESULT 4
AA09489/c
ID AA09489 standard; DNA; 1161 BP.
XX
XX AA09489;
AC
XX
DT 27-AUG-2003 (revised)
DT 28-FEB-1996 (first entry)
XX
XX 3 hydroxy-beta-ionone ring methylene to keto converting peptide DNA.
XX Xanthophyll; astaxanthine; methylene; keto group; conversion;
XX 3-hydroxy-beta-ionone ring;
XX Agrobacterium aurantiacum.
XX
XX
FH Key Location/Qualifiers
FT 1. 1161
FT /tag= a
FT /product= "beta-ionone ring 4-methylene_to_4-keto
FT _group_converting_polypeptide."
PN MO9518220-A1.
XX
XX 06-JUL-1995.
PD
XX
PF 26-DEC-1994; 94WO-JP002220.


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QY 1 TCATGCTCTCTCTGAGCAGAGGAGGCGTTTCGAGCAGGACGCGCCTGCGACAGCG 60
DB 1161 TCATGCTCTCTCTGAGCAGAGGAGGCGTTTCGAGCAGGACGCGCCTGCGACAGCG 1102
QY 61 AATGAGGCGGCGCTCGGTCGATGCGAAGCCGCGTGGCCATATGTCAGGCGCCGCGATA 120
DB 1101 AATGAGGCGGCTCGGTCGATGCGCAGCTGATCCGCGACGCTGACGCGCGCGGATTA 1042
QY 121 GAAGCGCTGATGAGCGGCGTGGCGAGGCGTGAACCGCTGAGAGCGATAGGACG 180
DB 1041 GAAGCGCTGATGATGTCATGCGGCAATGCGGTGAACCGCTGAGAGCGATAGGACG 982
QY 181 GTCGAGCGGAGCAGCGCGGAAACAGATCCGTTTACAGCGCGGAGAGAGCGGTCCGATC 240
DB 981 GTCGAGCGGAGCAGCGCGGAAACAGATCCGTTTCAAAAGCGGAAAGCGGTCCGCGG 922
QY 241 CCGCGGATGATGAGCGCGCAGCGCGGACCGCGGACG-----GGCGGACGCGGTCTAG 294
DB 921 CCGCGGATGATGAGCGCGTAAATCGCGATGCGCGCGCGCGCGCGCGTCCGATCCGCGCGCG 862
QY 295 GTCGCGCGCGCGATGCGATCCGCGGACCTGCGCGGATAGGAGAGGAAATATCCGTTGAC 354
DB 861 GAGCAGACCCCGCACCACTGCGCGACCTGTCGATAGGAGGAGGAAATAGCGGTGAC 802
QY 355 GAGGATGAAACAGCGCTGCGCGCGGACCGGACCGCGCGCGCGCGCGTGGTCCGCGCA 414
DB 801 CGGATGAAAGAACCCCGCGCGCGGACGCTCCAGCGGAAACGCGCGCGCGCGCGTGGTCC 742
QY 415 GAAGCTTATGCGCTCATGAGCGCGCAGCGGATGAGGAGGATGCGCTTTCGCGCGCATCTC 474
DB 741 GAAGCGCGCGCATCATGAGGCGCGCGGATGAGGAGGATGCGCGCTTTCGCGCGCATCTC 682
QY 475 CTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 534
DB 681 GCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 622
QY 535 GTTCAGATGCGCGCGCGCTGCTGAGCGCGGATCTCTGATCAGGATCGGAGTGGAGTGA 594
DB 621 GTTCAGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 562
QY 595 GGGCAGCAGATGATGATGAGCGGATGAGCGGATGAGCGGATGAGCGGATGAGCGGAT 654
DB 561 GGGCAGCAGATGATGATGAGCGGATGAGCGGATGAGCGGATGAGCGGATGAGCGGAT 502
QY 655 CGGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 714
DB 501 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 442
QY 715 ACCCAGGTCAGGTCGCGGCGCTGCGAGCGGACCGAGCGGCGTGCATCAGCGAGCGACGTC 774
DB 441 ACCCAGGTCAGGTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 382
QY 775 GATCCGCGAGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 834
DB 381 GATCCGCGAGTCGCGAGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 322
QY 835 CCAAGCGCAGATGACACCTCGACGACG-----CGATGAGCGCGCGCGCGCGCGCG 888
DB 321 CCAAGCGCAGATGACACCTCGACGACG-----CGATGAGCGCGCGCGCGCGCGCG 262
QY 889 GCGATGAGCTGTCGTCAGAGCGGCGGCGGATGTCGAGGAAACGAGCGCTCGATCCGTCGA 948
DB 261 CCGCTGATGAGCTGTCGTCAGAGCGGCGGCGGATGTCGAGGAAACGAGCGCTCGATCC 202
QY 949 TTTCGCGCGCAGGATGAGGCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1008
DB 201 GTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 142
QY 1009 GAGAGCAGAGTGTCTGTGTCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1068
DB 141 GAGAGCAGAGTGTCTGTGTCGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 82
QY 1069 ATCCGCTGCGGTCGCGAAGCGCGAGCGGATCAGCGCAGCGGACCGCGCGCGCGCG 1128

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DB 81 GTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 22
QY 1129 GATCAGCAGATCATGCTCTCA 1148
DB 21 CAGCAGCAGCTCATGCTCTCA 2

RESULT 7
AD096933/c
ID AD096933 standard; DNA; 1966 BP.
XX
AC AD096933;
XX
DT 23-SEP-2004 (first entry)
XX
DE CrtWcrty nucleotide sequence.
XX
KM carotenoid; transgenic plant; overlapping extension PCR amplification;
KM PCR; crtB; crtI; crtW; crtZ; astaxanthin; carotene;
KM grain crop; vegetable; crtWcrty; gene; de.
XX
OS Unidentified.
XX
PN CN1380415-A.
XX
PD 20-NOV-2002.
XX
PF 06-APR-2001; 2001CN-00105878.
XX
PR 06-APR-2001; 2001CN-00105878.
XX
PA (SHAN-) SHANGHAI YONGYE NONKO BIO ENG CO LTD.
XX
PI Yao Q, Peng R, Xiong A;
XX
DR MPI; 2003-230997/23.
XX
DR P-PSDB; AD096834.
XX
PT Synthesis of related gene for producing carotenoid in transgenic plant,
XX useful for improving quality of grain crops and vegetable.
XX
PS Example 1; Fig 1-2; 36pp; Chinese.
XX
CC The present invention relates to a related gene for producing carotenoid
CC in transgenic plant. The invention utilizes an overlapping extension PCR
CC amplification process and uses six genes of crtB, crtI, crtW, crtZ
CC and crtZ as templates to synthesize the related gene for synthesizing
CC astaxanthin with plant preference code and can make a synthetic gene for
CC expression in a plant to produce the carotene substances of astaxanthin.
CC The synthetic gene can be used to improve the quality of grain crops and
CC vegetables. The present sequence represents a specifically claimed
CC crtWcrty nucleotide sequence, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 1966 BP; 507 A; 721 C; 416 G; 322 T; 0 U; 0 Other;

Query Match 34.4%; Score 395.4; DB 11; Length 1966;
Best Local Similarity 60.1%; Pred. No. 3,6e-65;
Matches 698; Conservative 0; Mismatches 451; Indels 12; Gaps 2;

DB 1 TCATGCTCTCTCTGAGCAGAGGAGGCGTTTCGAGCAGGACGCGCCTGCGACAGCG 60
DB 1958 TTATGCGTTTCTTCTGAGAGAGTGTCTTCTGAGAGCGATCTGATTCGCGTCCGAGTGG 1899
QY 61 AATGAGGCGGCGCTCGGTCGATGCGAAGCCGCGTGGCCATATGTCAGGCGCCGCGATA 120
DB 1898 GATTCGTCGCTTCCGCGTGCATCTGATGTCGTCGAGAGAGTCTACCTGCGTA 1839
QY 121 GAAGCGCTGATGATGAGCGGCTGCGGAGGCGGTAACCGCTGAGAGCGGATAGGACG 180
DB 1838 GAATCTTTCAGAGAGACCGTGTGAGCTCTTTCGAGAGAGGAGTATCTTCT 1779

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OY	181	GTCCGGGGGGGAGCCGGGAAAACAGATCCGGTTACGACCGGCAAGAAACGGTCCGCATC	240
Db	1778	GTCCTGTCGAGACCTCTGAAGAGACATTCCTTGAGAGACTGAGAAATCTGTCTCTTCT	1719
OY	241	CCCGCGATCGATGCGCCCAAGCCGCGCACCGC-----GGACCGGGCGAGCCGGTGTCTAG	294
Db	1718	TGCTCTGTGATGCGTAGTCTCTGATTGACACTCTGAGTGCCTGCGTCCGGTGGGAC	1659
OY	295	GTCGCGCCCGCGATGCGATCCGGAACCTGGCGCGCATAGGGCAGCGCAATATCCGGTAC	354
Db	1658	GGAGAGACCTTGAGAGAGCTGTCGACATCTTGCTGCGATGAGGAGAGTACCGGTAC	1599
OY	355	GGGGGTGAACAGCCCTGCCCCAGCCCAACCGGCACCGCCCCCTGCGGTGTGCGCCA	414
Db	1598	TGGGTGGAAGAAGCCTGTCTGAGACCGACTGGAGCTGGACCTTCTGCTGTGTGCCA	1539
OY	415	GAAGCTTATGGCGTCATGGGCGCAGCGCATGGGACAGATGCCCTTTTGGCCCGCATCTC	474
Db	1538	GAACCTCTCTCGTGTGTGGAGGCGCATTTGGGAGATGCTCTTCTCTTCTGACCTTC	1479
OY	475	CTGCCCGGTTCAGAGCCCGCGCTGGGGGATGATGCAAGCAAGCCCTGCGCAGCGGCCATC	534
Db	1478	TGCACCGGTTCAGAGCTTGTGTCTTGGCTGATCTTGGATGCTGTGCGAGTGGCTCTC	1419
OY	535	GTCAGATCGCCCGCGCTGTGTAGCGGTATCTCTGATCAGATGCGGGTGGACATGAA	594
Db	1418	GTCGAGGTGCGCCGCGCTGAGATATCTGTGTCTTGCATGAGGATTCGTGTTCTGGAAA	1359
OY	595	GGGACGACGATATGATGAAGCCGTACCCGTCCATCTGCGGAAACGGTGGCTCATGATCAT	654
Db	1358	TGGGAGGAGTATGAAAGACGTACCGCTCTCTTGGGTGAGAGGGCGCTGCATGATATAC	1299
OY	655	CGGCGCTCTGACGCGCATGGGGGGCGTCCGTCTCGATCTCGACGCCACGAATTCCTGGA	714
Db	1298	TGGTCTTGGGACACCGCTGAGGTCTGTGCGTTTCATTTGCAACACGAGAACTTGGA	1239
OY	715	AACCAAGGTCAAGTCCGGGGTCTCGACGGCACACGCGGCTTCGATCAAGCAGGACCTC	774
Db	1238	GCCGAGGGTGAAGTGTCTGATATGGGTGTGGGCTCTGTGCCGTGAGAGAGGAGCCGTTC	1179
OY	775	GATCCGGCAGCCGTCGTCAAGCGTGCAGCGGATCTGTCAGAGCTCGGACATGCGTAT	834
Db	1178	GATTTTAACTACCGCAGAGAGGGTTGCACTTTGTGCTGAGAGTGCAGATGTCCGATC	1119
OY	835	CCACCGCAGATCGACACC-----CTGCAGCAGACCCCGATCAGCGGCCCGCTCGATGA	888
Db	1118	CCATCTGATTTCTGCACCGGATCTGACACATGCTGCTCGAGTGTGACACGTCGAGGGA	1059
OY	889	GCCATAGCTGTCTGTCAGCGCGCGGAAATGTGTGGGAAACCGACACTCTGATCCGTCA	948
Db	1058	GCCGTAGCCGTTGGAGCTTCTTGGCGTCTTGGGAATCTGATTTCTTGGTCTGGGCA	999
OY	949	TTCCGCGGACGAAATGGCGCAGCGCGCGCCAGCATTCGGGCGCAAAATCCGTGCTGTG	1008
Db	998	GTTTGCTCTTCTGAATGGTTGAAGCTTGTGCAGACAGTGTGGGAGAGAGTCTGGGTCTG	939
OY	1009	GCAGGACCAAGTGTCTGTGTTCCGAGGGGCGGACCGCGCGTGTAGACATCAAGATGCGGC	1068
Db	938	GCAGGACCAAGGTGTACCTTCGATGAGACCTGTCTGCTGTGTGTGAGAGAGACTCTTAG	879
OY	1069	ATCCGGTCTGGGGTGTGCGAAGCGCAAGGCGCATTCAGCGCACCGCACGCCCGCGCCG	1128
Db	878	GTCCTGTCTTGTGCTCTGAGTGGCAGTGTGCAATGAGACCGTTTGGAGACTGTCACTGTG	819
OY	1129	GATCAGCAGATCATGGCTCAT 1149	
Db	818	GAGAGGACAGTGTGTGATCAT 798	

AC	ADQ96833;
XX	
DT	23-SEP-2004 (first entry)
XX	
DE	crtWcrtY nucleotide sequence.
XX	
KM	carotenoid; transgenic plant; overlapping extension PCR amplification;
KM	PCR; crtB; crtI; crtW; crtZ; astaxanthin; carotene;
KM	grain crop; vegetable; crtWcrtY; gene; ds.
XX	
OS	Unidentified.
XX	
FH	Key Location/Qualifiers
FT	1..1944
CDS	/tag= a
FT	/product= "crtWcrtY"
FT	
PN	CN1380415-A.
PD	20-NOV-2002.
XX	
PF	06-APR-2001; 2001CN-00105878.
XX	
PR	06-APR-2001; 2001CN-00105878.
XX	
PA	(SHAN-) SHANGHAI YONGYE NONGKO BIO ENG CO LTD.
XX	
PI	Yao Q, Peng R, Xiong A;
XX	
DR	MPI: 2003-230997/23.
XX	P-PsDB; ADQ96834.
PT	Synthesis of related gene for producing carotenoid in transgenic plant,
XX	useful for improving quality of grain crops and vegetable.
PS	Claim 2; Page 1-2; 36pp; Chinese.
XX	
CC	The present invention relates to a related gene for producing carotenoid
CC	in transgenic plant. The invention utilizes an overlapping extension PCR
CC	amplification process and uses six genes of crtB, crtI, crtW, crtY
CC	and crtZ as templates to synthesise the related gene for synthesising
CC	astaxanthin with plant preference code and can make a synthetic gene for
CC	expression in a plant to produce the carotene substances of astaxanthin.
CC	The synthetic gene can be used to improve the quality of grain crops and
CC	vegetables. The present sequence represents a specifically claimed
CC	crtWcrtY nucleotide sequence, which is used in the exemplification of the
XX	present invention.
XX	
SO	Sequence 1944 BP; 497 A; 716 C; 412 G; 319 T; 0 U; 0 Other;
	Query Match 34.3%; Score 394; DB 11; Length 1944;
	Best Local Similarity 60.1%; Pred. No. 6.7e-65;
	Matches 696; Conservative 0; Mismatches 450; Indels 12; Gaps 2;
OY	4 TGCTTCCTCCGACAGCGGGCGGTTCGGCAGCGGCCTGCGCACGCCGAAT 63
Db	1944 TCGCTTTTCCCTTGAGAGATGCTCTTTCTGGAGGCACTGAATTGCGGTCCGAAATGGCAT 1885
OY	64 GGGCGGGCGGTCCGCTGACGATCGAAGCCGGTGGCCAAATCTAGGCGCCCCGGCATGAA 123
Db	1884 TGGTGGCTTTCGGGAGCAATTCTGAGTTGGTCTGCCAGCGAGAAGTCACTCGGTGAAA 1825
OY	124 GGCTTCGATTCAGCGGCTTCGGCAGCGGTAAACCCTGCGACGAGGGGATGAGCAAGGTC 183
Db	1824 TCTTTGATGAGAACCGTGTGGCATTTCTGTAGACTTTTGGAGGAGGGGTATTCCTTCTGTC 17655
OY	184 GGGCGGGCAGCGCGCGAACAACATCCGTTTAGACAGCGCAGGAAGCGGTGCGATCGC 243
Db	1764 TGGTGGCAGGCTCTGAAAGACATTTCTTTAGGAGTCTGAGAAATGCTCTTCTTCTTCG 1705
OY	244 GCGATGATGGCCGACCGCGCACCGC-----GCGACGGCGGACCGCGGTCTCAGAGTC 297
Db	1704 TCTGTGATTCGATGATCTCTGATTTGACACTCTAAGTGCCTGCGGTGCTGTGAGACCGGA 1645

QY 298 GCGCGCGGATGATCGGACCTGCGGATGAGGACGAGATATCCGGTGAACGG 357
 DB 1644 GAGACCTGCGACGACCTCTGCCACTTGTCTGCTGATAGGAGGAGTACCGGTGACTG 1585
 QY 358 GTGGAACAGCCCTGCCCCAGCCCAACCGGACCGCCCTGCGCGTGTGCGCGCAAA 417
 DB 1584 GTGGAAGAACCTGCTCTGAGACCGACTGGACCTTCTGCTGCTGCTGCTGCTG 1525
 QY 418 GCTTATGAGGTCAATGAGGACGAGCGGATGAGGAGGAGGAGGAGGAGGAGGAG 477
 DB 1524 ACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1465
 QY 478 CCGGATCGACCCCGCGCGCGGATGATGACGAGCGCTGCGCGAGCGCGCGCATGCTC 537
 DB 1464 ACCGATCGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1405
 QY 538 CAGATCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
 DB 1404 GAGGTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1345
 QY 598 CAGCAGATGATGAGGAGCGGATCCCGTCAATGCGGAGAGGCTGCTGCTGCTGCTG 657
 DB 1344 GAGGAGGTGATGAGGAGCGGATCCCGTCAATGCGGAGAGGCTGCTGCTGCTGCTG 1285
 QY 658 GCGCTGACGCGCATGAGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
 DB 1284 TCTTGGGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1225
 QY 718 CACGCTGAGGTGCGGAGGCTGCTGCAACGACCAACCGGCGCTGCTGCTGCTGCTGCT 777
 DB 1224 GAGGAGGTGATGAGGAGCGGATCCCGTCAATGCGGAGAGGCTGCTGCTGCTGCTG 1165
 QY 778 CCGGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 837
 DB 1164 TCTAGTACCGGACGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1105
 QY 838 CCGGATGACGACCC-----CTGCGACGACCGCGCATGACGCGCGCGCTGCTGCTG 891
 DB 1104 TCTGATTTCTGCAACCGGATCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1045
 QY 892 ATAGCTGCTGCTGACGCGCGCGGATGCTGCGGAAACCGGACCTCTGCTGCTGCTGCT 951
 DB 1044 GTAGCGGCTTGGGAGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 985
 QY 952 GCGCGGACGATGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1011
 DB 984 TCTCTTCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 925
 QY 1012 GAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1071
 DB 924 GAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 865
 QY 1072 CCGTCTGCGGCTGCGGACGCGGACGCGGATGACGCGGACGCGGACGCGGACGCGG 1131
 DB 864 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 805
 QY 1132 CAGCAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1149
 DB 804 GAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787
 RESULT 9
 ADC99013/c
 ID ADC99013 standard; DNA; 1185 BP.
 AC ADC99013;
 XX
 XX
 DT 01-JAN-2004 (first entry)
 XX
 XX Bradyrhizobium sp crry DNA.
 KW gene cluster; canthaxanthin biosynthesis; carotenoid; astaxanthin;

KW poultry; fish feed; crry; ds.
 XX
 OS Bradyrhizobium sp.
 XX
 PN US2003087337-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 11-JUN-2002; 2002US-00166037.
 XX
 PR 12-JUN-2001; 2001US-0297272P.
 XX
 PA (GIRA/) GIRAUD E.
 XX (HANN/) HANNIBAL L.
 PI Giraud E, Hannibal L;
 XX
 DR WPI; 2003-777219/73.
 XX
 PT Novel isolated gene cluster involved in canthaxanthin biosynthesis,
 PT having crry, crrt, crtB and crtW genes clustered in this order, in the
 PT same orientation, and crtB preceding 4 genes in the opposite direction.
 XX
 PS Claim 6; SEQ ID NO 2; 14pp; English.
 XX
 CC The invention relates to a novel isolated gene cluster involved in
 CC canthaxanthin biosynthesis comprising a polynucleotide in which crry,
 CC crtI, crtB and crtW genes are clustered in this order and in the same
 CC orientation and the crtE gene is oriented in the opposite direction. The
 CC polynucleotide of the invention may be useful for producing at least one
 CC carotenoid such as astaxanthin or canthaxanthin which may be used within
 CC poultry or fish feed. The current sequence is that of the Bradyrhizobium
 CC sp. crry DNA of the invention.
 SQ Sequence 1185 BP; 169 A; 414 C; 390 G; 212 T; 0 U; 0 Other;
 XX
 Query Match 20.6%; Score 236.4; DB 10; Length 1185;
 Best Local Similarity 54.0%; Pred. No. 2.5e-35;
 Matches 589; Conservative 0; Mismatches 471; Indels 30; Gaps 4;
 QY 78 TGACGATGGAAGCCGCTGCGGCAATGTCAGGCGCGCGCGCATAGAGCGCTGATCAGCG 137
 DB 1102 TGAGACGCGGCGAGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1043
 QY 138 GCTGCGGCGAGGCGGTGAGAACCGCTGCAAGCGCGATGAGCGGTGCGGCGGCGCGCG 197
 DB 1042 CCTGATCGAGACCGTAAATGCTGCGCAGATTCGCTGAGCGCTCGAGAGGCTGCGGCGCT 983
 QY 198 GGAACGACATCCGCTTCAAGACGCGCAGAGAGCGGTGCGGATCCGCGCGATGAGCGCC 257
 DB 982 TGAAACGACATCCGCTTCAAGAGCGATGATGATGATGATGATGATGATGATGATGATG 923
 QY 258 AGCCGCGCACCGCGCGGAGCGGCGGAGCGCGGTGCTGAGGTG-----CGCG 302
 DB 922 AGCCATGATGCTGCTGCGCGCGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 863
 QY 303 CCGGATGAGCATCCCGGACCTGCGCGGATGAGGCGAGGAGATATCCGCTGAGCGGCTGGA 362
 DB 862 CCGTACGAGATCGCGGAGCGGAGCGGCGGCTCGGCGAGGAGATGCGGTGCTGATGGA 803
 QY 363 ACAGCCGCGCGCGCGGAGCGGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTA 422
 DB 802 CGAGAGGCGCGCGGAGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 746
 QY 423 TGGCGTCAATGAGCGCGGATGAGGCGGAGATGCGCTTTCGCGCGCGCATCTCTCCCGG 482
 DB 745 ACGATGCGCGCGCGGAGATGAGCGGCGGAGCAACCTGCTCGCGCGGATGATCTCGGCGA 686
 QY 483 TTCAGCCCGCGCTGCGG---GATATGCAAGGAGCGCTGCGCGCGCGCGCGCATGTGTCA 539
 DB 685 TCTGCGACCGCTTGGCGAGCGGCTGAGCGCGGAGTGGATGAGGAGCACTGCTCGGCGCA 626
 QY 540 GATCCCGCGCGCTGCTGAGCGCGGATCTGATCAGATGAGGAGTGGAGTGAAGGCA 599

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Db 625 ACTCCCGCCGCTGCTATGAGTGTCTTCATCAACGCGCTGAGGCTGACCGCA 566
QY 600 GCAGATAGATGAAGCGGTACCCGCTCATCTGCGGAAACGGTCCGATCATGATCGGAC 659
Db 565 GCGTGTAGACGAAGCGATAGCCGCTCTGCGCGACCGTCCGCTTCATCAGATGGGCA 506
QY 660 GCTCGACCGCATGAGGCGGCGGTGCTGATCTGACGCCCAAGATTTCTGAAACCA 719
Db 505 CATCGAGGCGGTGCGCGCGCGCGACCGCACTTCGAGCCCGAAGACTTCTGAACCGCA 446
QY 720 CGGTACAGTGGGGGCTCTGACGCAACCGGCGCTTCATTCAGAGGAGCTTGATCC 779
Db 445 GAGCGAGCGCCCGCACCCGCGCGCGCGCGCATGATCAAGAGGCGCGCGCAAG 386
QY 780 GCGAGCGCGCTGCTGACG-----GTGCGCGCGTATCTGTCAGCGCTGCGACATGCG 830
Db 385 TGCGGCGCGCTCTCCAGACGACATGCTGCTGCGGTGCGAGATGCGCGCTGCGCGCA 326
QY 831 TATTCACCGCATGACACCCCTGACGACGCCCATTCAGCGCGCGCGCTTGATCGAGC 890
Db 325 GGATCCTCTCGGAAAGCGCTGCTGACCTCGGACGCGCGCGCTGACGCTCATGAGCA 266
QY 891 CATGACCTGTGCTGACGCGCGCGCGCATGCTGCGGAAACCGCACTTCTGATCCGTCATT 950
Db 265 GGTAGGCGGTGACACGACGATGCGCATGTTGCGCGAAGCGCACTTCATTAACCGCGCACG 206
QY 951 CGCGCGACGATGAGGCGGACGAGCGCGCGCGCATTCGCGGAAAGATCGTGTGCTGCG 1010
Db 205 GATGACCGACGAGCGCTGCGAGCGCGCGCTGCTGCTGCGACGAGATGCTGCTCAAGAA 146
QY 1011 AGGACCGAGTGTGCTGCTCGAGGCGCGCGCGCATTCGCGGACATCAAGTGCAGCAT 1070
Db 145 AGCTCAAGGTGTGATGTTGCGCGGATGCTGCGCGAGCTTCGATGATGACGACGCGCAAT 86
QY 1071 CCGGCTGCGGTGCTGCGGACGCGGACGCGCATTCAGGCGACCGCGCGCGCGCGCA 1130
Db 85 CCGGCGCGGTGCTGCTGCTGAGCGCGCAAGCGCATGACGCGCGCGCGCGCGCATGA 26
QY 1131 TCAGCAGATC 1140
Db 25 CGATGACGTC 16

RESULT 10
ADM9859/c
ID ADM98599 strand: DNA; 12753 BP.
AC ADM98599;
XX
XX 01-JUL-2004 (first entry)
DE Geranylgeranyl pyrophosphate synthase DNA #19.
XX
XX Geranylgeranyl pyrophosphate synthase; gene; ds; diterpene;
KM diterpene precursor; diterpene synthase; defence toxin;
KW volatile defensive signal; pollinator attractant; photoprotectant.
XX
OS Pantoea agglomerans.
XX
XX US2004072323-A1.
XX
XX 15-APR-2004.
XX
XX 07-JAN-2002; 2002US-00041018.
XX
XX 05-JAN-2001; 2001US-0259880P.
XX
XX (MATS/) MATSUDA S P T.
XX
XX (HART/) HART E A.
XX
XX Matsuda SPT, Hart EA;
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DR WPI; 2004-373921/35.
XX
XX New unicellular organisms comprising exogenous nucleic acids encoding a
PT geranylgeranyl pyrophosphate and a diterpene synthase, useful for
PT producing diterpenes and diterpene precursors.
XX
XX Claim 2; SEQ ID NO 19; 38bp; English.
XX
XX The invention relates to a unicellular organism for producing a diterpene
CC or diterpene precursor comprising an exogenous nucleic acid sequence
CC encoding a geranylgeranyl pyrophosphate synthase under the control of a
CC promoter operable in the organism, and an exogenous nucleic acid sequence
CC encoding a diterpene synthase under the control of a promoter operable in
CC the organism. The invention also relates to methods of producing a
CC diterpene or diterpene precursor and a method of isolating a diterpene
CC synthase comprising growing several cells in the presence of a
CC polycyclic resin to make a cell/resin mixture, where at least one of
CC the cells further comprises at least one isolated and purified nucleic
CC acid sequence of a yeast expression library, and the expression of the
CC nucleic acid sequence is regulated by an inducible promoter under
CC conditions where the expression is induced, filtering the cell/resin
CC mixture, extracting the cell/resin mixture with alcohol to produce an
CC organic eluent and analysing the organic eluent by a screening method
CC including chromatography and/or spectroscopy, to identify the nucleic
CC acid sequence encoding the diterpene synthase. The unicellular
CC microorganism is useful as a diterpene or diterpene precursor producing
CC system. Diterpenes, in plants, serve as defence toxins, volatile
CC defensive signals, pollinator attractants and photoprotectants. This
CC sequence represents DNA encoding a geranylgeranyl pyrophosphate synthase
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
SQ Sequence 12753 BP; 2489 A; 3880 C; 3911 G; 2473 T; 0 U; 0 Other;

Query_Match 18.6%; Score 213.4; DB 12; Length 12753;
Best Local Similarity 52.1%; Pred. No. 5.1e-31;
Matches 581; Conservative 0; Mismatches 516; Indels 18; Gaps 4;

QY 41 CGACGCGCTGCGACGCGGATGAGCGCGGCTGCGTGAAGATCGAAGCGGCTGCGCC 100
Db 7916 CGCCAGGCTTGCGCCGAGGAAACCGGTGCTGCGCGTCAAAATCGGCGCTTACAAAG 7857
QY 101 AATGTACGCGCGCGCATGAAAGCTGATCAAGCGCTGCGGCGCGGATGAACGCC 160
Db 7856 AGAGAGACCGACCGCGCTAAAGCGCTTACGAGGCGCTCGGACGCCATTAAGCGCG 7797
QY 161 TGACAGAGCGATGACGAGCGGTGCGGCGCGGACCGCGGAAACGATCGGTTACGAGC 220
Db 7796 TGATCACCGCGACGCGGCTTCTCTGCGCGCGCGCGGCAAGAAAGATCGGTTACGAGG 7737
QY 221 CGCAGGAAAGC---GGTCCGATTCGCGGATGAGCGCGCGCGCGCGCGCGCGCG 277
Db 7736 CGGAGGATTCCTGCTGCTGCGCAAGTGGCGTTGCGAAACTCGCGGTAGCTGATGAGC 7677
QY 278 GCGACGCGGTGCTGAGTGGCGCGCGCGGATGAGTCCGACCTGCGGCGCATAGGCG 337
Db 7676 GGAACGCTGCCAGCGCGGCGGTGCGCAATCGGTCGCGAAGGCGCACCGCGCACCG 7617
QY 338 AGCGAATTCGAGTACGCGGTGGAACAGCCCTGCGCGCGCGCGCGCGCGCGCGCG 397
Db 7616 AGCGAATGACGATGATGAGGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7557
QY 398 TGCGGTGCTGCGCGCGCGGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 457
Db 7556 GCGCATGCGC---CCACAGAGCTGATGTCACCGCGCGCGCGCGCGCGCGCGCGCG 7500
QY 458 CTT---TGCGCGCGCATCTCTGCGCGGTGACGCGCGCGCGCGCGCATAGTCCAGCA 514
Db 7499 GTCTCTGCGGTTCAGGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTAAC 7440
QY 515 GCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 574
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Db      7439 GTCGTGCGTAGGCGATTATATCATCCGTCGCGGACATTTGGCCGTAGCCGTATCTTCGATC 7380
QY      575 AGGATGCGGTGGGAGTGAAGGCGACAGATAGATGAAGCGGTAACCGGTCCATCTGCGGA 634
Db      7379 AGCAGCGGTGCGCGAGAGCGGACGCTGTAGACAAAGGATAGCCCTGCTGCTCGCC 7320
QY      635 ACCGTGCGCTTCATGATTCATTCGCGCCCTCGACCCCAATGGGGGCGCTGCTTCGATCTCG 694
Db      7319 ACCGTGGATTCATTCAGATTCGATAGCGTACAGCCCGTGGGCGTGTGTCAGCCGCCACTCG 7260
QY      695 AGCCCAAGAAATTTCTGAAACCCACAGGTACAGTGGGGGTCTCGACGGCACCAAGCGGCG 754
Db      7259 TGAACAAGAAAGCTGATAGCCGCTTGTGATCGCGAACTGCGGCTTCACGCCGCTTCGCG 7200
QY      755 TGATACACGAGGACCTTCGATCCGCGAGCCGCTCGCTGACGCTGCGCGCGGATGATGTC 814
Db      7199 TCAATACCGCTCCGCGAAGCAGCGCTTACCGTTGCAAGGCGCACGCTATTGGGTAA 7140
QY      815 AGCGTCGCGACATGCTATTCACCGCGACATCGACACC-----TGCACGACCGCG 865
Db      7139 ACCTGCTCACCAGAACAGTTTACCAAGTTTCTCCCGACGCCCTGATGCGAGGGCTCG 7080
QY      866 ATCAGCGCGCCGCTTCGATCGAGCAATAGCTGTGTCAGCGCGGCGCAATGCTCGGA 925
Db      7079 GCAAAAGCGCTGAGGTAATGAGTAGTACCGCGCGCGAGCGCGCAAGATCGGGA 7020
QY      926 AAGCGACCTTCCTGATTCCTTCATTTGGCGCGACAGATGGGCGCACAGCGCGCCACCAT 985
Db      7019 AACTGACCTCATAGCCCGCGCGAGGCTGGGCCACACAGCGCGGCGCAAGCGGCTCTGC 6960
QY      986 TCGGCGAAAGATCCGCTGTGTCGACGAGACAGATGCTGTGTCGACGAGCGCGACCGC 1045
Db      6959 CCGGAGTCAATGCTTCTTATGAAATGACCAAGTATGTTCCCGCGGCTGCTCCCG 6900
QY      1046 GCGTCGAGCATCAAGTGCAGCGCATCCGCTGTCGCGTGGCAACGGCAAGCGGATCAGC 1105
Db      6899 GCGTCGATCAAGCAGGATTAAGCTGGGGTAGCGCTGGGCGAGAGCGGATCAGC 6840
QY      1106 GCACCGGACAGCCCGCGCGCGCGATCAGCATC 1140
Db      6839 CCGTTGCGCAGCGCGCGCGCATTAATAATCATGATC 6805

RESULT 11
AAD3511/c
ID      AAD3511 standard; DNA; 1149 BP.
AC      AAD3511;
XX
XX
DT      25-JUL-2002 (first entry)
XX
DE      Pantoea stewartii lycopene cyclase (CrtY) gene.
XX
XX      Carotenoid; isopentenyl pyrophosphate; antheraxanthin; dieter;
KM      anti-oxidant; steroid; flavour; fragrance; electro-optic application;
KM      aquaculture; enzyme; lycopene cyclase; CrtY; gene; ds.
XX
XX      Pantoea stewartii.
OS
XX
XX      Key      Location/Qualifiers
FH      CDS      1..1149
FT      /tag= a
FT      /product= "CrtY protein"
XX
XX      MO200218617-A2.
XX
XX      07-MAR-2002.
XX
XX      04-SEP-2001; 2001MO-US027420.
XX
XX      01-SEP-2000; 2000US-0229858P.
XX      01-SEP-2000; 2000US-0229907P.
XX

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PA      (DUP0 ) DU PONT DE MEMOURS & CO E I.
XX
XX      Brzostowicz PC, Cheng O, Dicosimo DJ, Koffas M, Miller ES;
PI      Odum JM, Picataggio SK, Rouviere PE;
XX
XX      WPI; 2002-351711/38.
DR      P-PSDB; AAE22313.
XX
XX      Producing carotenoid compounds e.g. antheraxanthin and astatenanthin, by
PT      using microorganisms having a nucleic acid molecule encoding enzymes in
PT      the carotenoid biosynthetic pathway and which metabolize single carbon
PT      substrates.
XX
XX      Example 8; Page 138; 156pp; English.
XX
XX      The invention relates to a method for producing carotenoid compounds. The
CC      method comprises a transformed metabolizing host cell, comprising
CC      suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule
CC      encoding an enzyme in the carotenoid biosynthetic pathway, under the
CC      control of regulatory sequences, and contacting the host cell with carbon
CC      substrate to produce a carotenoid compound. The method is useful for
CC      producing carotenoid compounds such as antheraxanthin and astatenanthin, by
CC      using microorganisms having a nucleic acid molecule encoding enzymes in
CC      the carotenoid biosynthetic pathway and which metabolize single carbon
CC      substrates. The carotenoids have potent anti-oxidant properties useful in
CC      diet, and aquaculture elements. The carotenoids are also useful as
CC      intermediates in the synthesis of steroids flavours and fragrances and
CC      compounds for potential electro-optic applications. The present sequence
CC      is Pantoea stewartii lycopene cyclase (CrtY) enzyme gene used in the
CC      invention
XX
XX      Sequence 1149 BP; 228 A; 325 C; 315 G; 281 T; 0 U; 0 Other;
XX
XX      Query Match      18.3%; Score 209.8; DB 6; Length 1149;
XX      Best Local Similarity 51.8%; Pred. No. 2.5e-30;
XX      Matches 578; Conservative 0; Mismatches 522; Indels 15; Gaps 4;

QY      42 GCACGCGCTCGGACACGCGGAATGGCGGGCGTCCGGTGAAGATGCGAAGCCGGTGGGCA 101
Db      1123 GCATGCGCCGGAACCGGACCGGCGGCTTGCCTCAGATGCTGACCATGCGTCA 1064
QY      102 ATGTCAGCGCCCGCATAGAACCGCTCGATCAGCGGCTCGCGCAGCGGTAGAACCGCT 161
Db      1063 CGGTGAGTTTCCCGATTAAGCGGGCAATCAATTCGTGGGTAAAGCATGAACCGT 1004
QY      162 GCACGAGCGATAGCGACGCTGCGGGCGAGCGCGGACACGATCCGTTTACAGCGC 221
Db      1003 GCATCAACGCGCAGGCTGACTCGCGCGGTCCGGCTTAACAAACATGCGATTCAACATGC 944
QY      222 GCAGAGAGCGGTCCGATCCGCGCGATGATGATGCGCCAG---CGGCGACCGGCGAGCGG 278
Db      943 GGAAGAAACCTCTGTTGCTGCGCAACGTTGCTGGGCAAGAGAGCAATCGTTGTATACG 884
QY      279 CGACGCGGTCTCAGTGCAGCGCGCGCATGCGGATCCGCACTTGCAGCGGATAGGCGCA 338
Db      883 AGGAAGAGTTAAACATTCAGCGCGCTGAGACGATCGGCGACCGCGCAAGGAGGGA 824
QY      339 GCGAATATCCGATGACGCGGCTGAAACAGCCTTGCCTCCCAAGCCCAACCGGACCGCCCT 398
Db      823 GCGAGTAGCCGGTTGTCGATGAACAGCCCGCGCGTATCCGTTACAGGCTTGCAGTT 764
QY      399 GCGCGTGTGCGCGCAAGACCTATGCGCTCATGCGGCGAGCGCGCATGCGGAGATGCCCC 458
Db      763 GC-TGTTGCAAAATGACGATTAATTCGCGCTTAAGTATGAGGCAATGACCCCTGTTT- 706
QY      459 TTTGCGCGCATCTCTGCGCGGTTCAGCGCCCGCGCTGCGCGCATAGTCCAGCGAGCT 518
Db      705 -TTCCCGACGAACGCTCTTAACGCGCAACCTGTGCGGACGATATGCGAATGTTCT 647
QY      519 GCGCAGCGCGCATCTGTCAGATCGCGCGCTGCTGAGCGGTATCTTCATTCAGGA 578
Db      646 GACGCGCGCTTCCGCTGAAGATTAGCTTCTCATGATGATGATGCTTGCATCAGCA 587

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Oy	579	TGCGGCTGGGACTGAAGGGCAGACATGATGATGAAGCGGTACCCGTCATCTGCGGAACGG	638
Db	586	GTCGGCTTCGGAAAGCCGACGGGTATTAACAAAGCCGGTAGCCATTGGCTGATGACACGG	527
Oy	639	TCGCGTCCATGATCATTCGGGCGCTCGACGCCCATGCGGGGCGCTCGGTCCTGATCTCGACGC	698
Db	526	TCGATTCATGATTAATTCGGTAGCATTAACCATTCGGGCGCGCTCAGTTGCCACTCTTAGC	467
Oy	699	CCACGAATTTCTGGAACCCACGCTCAGGTGTCGGGGGTCTCGACGGGCACACGGGGGTGCA	758
Db	466	CGATTAATAGCTCGAATCTTAAGCGCTAGTCAGAAATCAGGGCGTGTAAACCCGTCGTCGA	407
Oy	759	TCACCCAGGACGCCCTCGATTCGCGACCGCTCCGTCAGCGTCCGCGCGTATGTCACAGCG	818
Db	406	TCACCTGTACTGGCATGAATTAATCCGGCCATCCGCTTACTCGACCGATTCAGCATGAACGG	347
Oy	819	TCGCGACATGCGTATTTCCACCGCATCGACACCTCTGCAGACCCCGCATCAGCGG----	874
Db	346	CTGAATACCGCGGTATGCAAGCCATTAATGTTGTCCAAACGTGTTGCCGAGGTATCCGGGCGA	287
Oy	875	-----CCGCGCTCGATTCAGACCCATAGCCTGTCTGTCAGCGCGCGCGAATGTCGGAAACG	929
Db	286	AATGCGGGAGGTTCACGACGATGATGACCACTGTTCACATGCGGACGCGCTTGCGGGAAAC	227
Db	226	GAACTCTGGTAGTCGGGCGCAGTATGACCAACAGCGCGCTATCCAGCGATCTGATTCA	167
Oy	990	GCGAAGATTCGCTGTGATGGCAGACCAAGTGTGCTGTGTCGAGGGGCGGACCGCGCGT	1041
Db	166	GCGTTAAATCTCTTCGTGTGAAGGACCAAGTATGTTGCTCCCTCCGCTCAGAACCCGCT	107
Oy	1050	CGAGCATCAAGATGCGCGCATCCGATCTGCGGTGCGGGAACGGCAAGCCGATCAGCGCAC	1104
Db	106	CAATAGACAAAGATCCGCATATCCGATGTGTTGCTGAAGCCGAGCGGATTAAGGCCAT	47
Oy	1110	CGGACAGCCCCCGCGCCCGCGATCAGACATCATGG	1144
Db	46	TAGCCAGACCGGACCCGACCAAGATGATCATAG	12
RESULT 12			
ABT14191/c			
ID	ABT14191	standard; DNA; 1149 BP.	
AC	ABT14191;		
XX	20-FEB-2003	(first entry)	
DT			
XX	Pantoea stewartii lycopene Beta-cyclase gene.		
DE			
XX	Gene; ds; carotenoid; crt.		
KW			
XX	Pantoea stewartii.		
OS			
XX	W0200279395-A2.		
PN			
XX	10-OCT-2002.		
PD			
XX	25-JAN-2002; 2002MO-US002124.		
PF			
XX	26-JAN-2001; 2001US-0264329P.		
PR	04-MAY-2001; 2001US-0288984P.		
XX			
XX	(CRGI) CARGILL INC.		
PA			
XX	De Souza ML, Kollmann SR, May CA, Schroeder WA;		
XX	MP1; 2003-075455/07.		
DR	P-PSDB; AAO16019.		
XX			
PT	Novel isolated nucleic acid useful e.g. to engineer host cells with the		
XX	ability to produce particular carotenoids and polypeptides useful in cell		

PT	-free systems to make particular carotenoids.
PS	Claim 81; Page 60; 74pp: English.
XX	
CC	The invention comprises the amino acid and coding sequence of a number of
CC	carotenoid (crt)-related proteins. The crt-related DNA and protein
CC	sequences of the invention are useful for engineering cells which are
CC	able to produce carotenoid. The present DNA sequence represents a crt-
CC	related gene of the invention
XX	
SQ	Sequence 1149 BP; 228 A; 325 C; 315 G; 281 T; 0 U; 0 Other;
	Query Match 18.3%; Score 209.8; DB 8; Length 1149;
	Best Local Similarity 51.8%; Pred. No. 2.5e-30;
	Matches 578; Conservative 0; Mismatches 522; Indels 15; Gaps 4
QY	42 GCACGGCTCTGCGACAGCAGGAATGGCGGGGCGTCCGGTAGCAATGCAGACCGCGGTGCGCCA 101
DB	1123 GCAAATGCCGGAAAACGGGAACGGGCGGCTTGCGCTCAGAATGGTAGCGATCGGTCA 106
QY	102 ATGTACGGCGCCCGCATMAAGCGCTTGATCAGCGGCTGGCGCAGGGGTTGAACCGGT 161
DB	1063 CGGTAGATTTCGCCGATMAAAGCGGGAATCAATCTCCGGTAGCGCATAGAAACGTT 100
QY	162 GCAGAGGCGGTAAGGAGACGTCGGCGGGGAGCGCGGAGACAGATCCGGTTACAGAGCC 221
DB	1003 GCATACACGCGCAGGTACTGTCGGCGGTCGGCTAAATAAACATGCGATTCACTATC 944
QY	222 GCAGGAACGGTCCGATCCGCGCGCATCGATGACCAG---CCGCGCACCGCGCAGCGG 278
DB	943 GGAAAAACCCCTGTGTCGCCACGTTCTGGGCAAACTGAGCAATCGTCTGTGTAACG 884
QY	279 CGGACGCGGTGTCAAGTCGCGCGCGCGATGAGCATCCGCGACTGCGCGCATAGGGCA 338
DB	883 AGGAAAGATGAACATCTCAGCGCGCTGAGACGATCGCGCACCGCCACCGGAGCGGTA 824
QY	339 GCGAATATCCCGTGAACGGGGTGGAAACAACCCCGCCCCAGCCCAACCGSACCGGCCCT 398
DB	823 GGGAGTACCCTGGTGTGCGATGAACAACCGCGCGGCTGTAATCCGTACAGGTTGCGGTT 764
QY	399 GCGCGTGTTCGCGCAGAAAGCCTTAGCGGTGATGAGGCCAGCGCATGAGGAGATGCCCC 458
DB	763 GC-TGTTGCCAAACTGACGATTAATGCCCGGTAAACGTAAATGGGCAATGCCACCTGTT- 706
QY	459 TTTCGCGCGGATCTCTGCGCGGTCAAGCCCCGCTCGAGCGGATAGTCCAGCGACGCT 518
DB	705 -TTCCCGCAGCAACGTCTGTAAACGGCCAAACCTGTGCGCAGCATAAATCGCGAATGTTCT 647
QY	519 GCGCCAGCGCGCATCTGTCAGATGCGCGCGCTGCTGTAAGGGCTAATCTTCGATCAGGA 578
DB	646 GACCGGCGCGTTCGCGCTGAAAGATTAGCTTGTCAATGATGATGTGTCTTCGATCAGGA 587
QY	579 TGCGGGTGGAGCTGAAGGCGACGACATATGATGAACCGGTACCCGCTCAATCTTCGGAACGG 638
DB	586 GTGCGGTTGCGGAAGCGGCGAGGGATTAACCAAAGCGGTAGCAATTTTGCTGATGAGACGG 527
QY	639 TCAGCTCATGATCATTCGCGCGCTTCGACGCCATGAGGGGCGCTCGGTTCTCGATCTCAGCGC 698
DB	526 TCGCATCATGATTAATTCGGTGAAGATTAACCATGCGGCGCGCTCAGTTGCCACTCCTGAC 467
QY	699 CCAGCAATTTTGTGAAGAACCCAGCGTCAAGTGGGGGTCTCGACGGCACCACGGGGGTGCA 758
DB	466 CGATMAATGCGCTGGAATCTTACGCGCTAGTGAATCAGGCGCTGTAAACCCCTCGTCTCA 407
QY	759 TCACGCGAGGACCCCTGATTCGCGGAGCGGCTCGTAGGGGTGCGCGCGGATGATGTCACAGG 818
DB	406 TCACGTGATCGCATGAATTAATTCGGGCAATTCGCTAATCGAACCGAATTCAGATGAACGG 347
QY	819 TCGCACATGCGTATTTCCACGCGAGATCGACACCTTCGACGACGCCGATCAACGCG--- 874
DB	346 CTGAATACCGCGGTATGCAACCATTAATGTGTGCTCAAACTGTTGCCGAGATATCCGGGCA 287
QY	875 ----CCGCGCTCGATCGAACCATTAAGCTGTGTCAGCGCGCGGCAATGCTGGGAACG 929

Db	286	ATATCCGGGAGGTCAACGAGATGATGACCTGTTTCACATGCGACGAGCGGTTGGGGGAAAC	227		
Oy	930	CGACCTCTCTGATCCGTCATTCGCGCGACGAGATGGGCGACAGGCGCGCCAGCCATTCCG	989		
Db	226	GAACCTGTGTAGTCGGGCGCAGATGATGACACAAAGGCGGCTATCATCAGAGATGCTGATTCA	167		
Oy	990	GCGAAGATCCGTGTCTGTGGCAGACCAAGGTGTGCTGATCCGAGGGGCGCGACCGCGGT	1049		
Db	166	GCGTTAAATCCCTCTTCGTGAAAGGACCAAGTATGGTTCTCTCCGCGCTCAGAGACCGCGCT	107		
Oy	1050	CGAGCATACGATGCGCGCATCCGGTCTGCGGTGCGGAGGCGAAGCGCGCATCGAGCGAC	1109		
Db	106	CAATAGCAAGATCCGATATCCGATCTGTTGCTGAAGCCGAGCGGCAATGAGCCAT	47		
Oy	1110	CGACAGCCCGCGCGCCGCGATCAGCAGCATATG	1144		
Db	46	TAGCCAGACGCGGACCGACGAGCAATGATCATATG	12		
RESULT 13					
AC	ACC44761/C	ACC44761 standard; DNA; 1149 BP.			
XX	ACC44761;				
DT	03-JUN-2003	(first entry)			
XX					
DE	Pantoea stewartii	lycopene cyclase encoding DNA SEQ ID NO:5.			
XX					
KM	Pantoea stewartii;	carotenoid biosynthetic enzyme; crtB; crtX; crtY;			
KM	crtI; crtB; crtZ; lycopene cyclase; enzyme; phytoene; carotenoid; gene;				
XX	ds.				
OS	Pantoea stewartii.				
XX					
FH	Key	Location/Qualifiers			
FT	CDS	1..1149			
FT		/*tag= a			
FT		/product= "lycopene cyclase (crtY)"			
FT		/note= "carotenoid biosynthetic enzyme"			
XX	MO2003016503-A2.				
XX	27-FEB-2003.				
XX	15-AUG-2002; 2002MO-US026647.				
XX	15-AUG-2001; 2001US-0312646P.				
XX	(DUPO) DU PONT DE NEMOURS & CO E. I.				
XX					
PI	Brostowicz PC, Cheng Q, Picatagaglio SK, Rouviere PE;				
XX	WPI; 2003-268323/26.				
DR	P-PSDB; ABP96687.				
PT	Novel nucleic acid molecule isolated from Pantoea stewartii encoding a				
XX	carotenoid biosynthetic enzyme, useful for regulating carotenoid				
XX	biosynthesis in an organism.				
XX	Claim 2; Page 60-61; 68pp; English.				
CC	The present invention describes Pantoea stewartii carotenoid biosynthetic				
CC	enzymes (I). More specifically described are the geranylgeranyl				
CC	pyrophosphate synthase (crtE), zeaxanthin glucosyl transferase (crtX),				
CC	lycopene cyclase (crtY), phytoene desaturase (crtI), phytoene synthase				
CC	(crtB) and beta-carotene hydroxylase (crtZ) enzymes (see ABP96685 to				
CC	ABP96690) encoded by ACC44759 to ACC44764. (I) can be used for regulating				
CC	carotenoid biosynthesis in an organism, by over-expressing (I) in an				
CC	organism, such that the carotenoid biosynthesis is altered in the				
CC	organism. (I) and the genes encoding (I) are useful for converting				
CC	phytoene to the carotenoids, for creating recombinant organisms that have				

Query Match	18.3%	Score 209.8	DB 8	Length 1149
Best Local Similarity	51.8%	Pred. No. 2.5e-30		
Matches	578	Conservative	0	Mismatches 522; Indels 15; Gaps 4
CC	the ability to produce various carotenoid compounds, and also for			
CC	enhancing or manipulating carotenoid compounds. (1) can also be used for			
CC	producing gene products having enhanced or altered activity			
XX				
XX	Sequence 1149 BP; 228 A; 325 C; 315 G; 281 T; 0 U; 0 Other;			
QY	42	GCACGGCCTGCGACACGCGGAATGAGGCGGGCGCGCTGCGATGCGAAGCCGCTCGACCA	101	
DB	1123	GCAATGCCGCCAATAACGGGAACGGCGCGCTTCCCGCTCAGAAATGGCTAGCCATCGCTCA	106	
QY	102	ATGTCAGGCGCCCGGCATAGAACGCTCTGCATCAGCGGCTGCGGACGGCGGTAAACCGCT	161	
DB	1063	CGGTAGATTTCGCGCATTAAGCGGGCAATCAATCTCGGGTAAAGCCATAGAAACGCT	100	
QY	162	GCACGAGCGCATAGCGAGGTGCGGGCGGGCGACCGCGGAACAGCATTCGGTTTCAGTAGCC	221	
DB	1003	GCATCACACGCGCAGGTGACTCTCGCGCGGTCCGGCTTAAACAACTGCGATTTCAGATGCG	944	
QY	222	GCAGGAACCGGTCGCGATCCGCGCGCATGATGATGAGCCAG---CGGCGACCGGCGCAGCGG	278	
DB	943	GGAAAAACCCCTGTTGCTGCTGCCACCTTCTGTGGCAAAATGAGCAATTCGTCTGTGTAACG	884	
QY	279	CGACACCGGTCGTCAGGTGCGCGCGCGCGCGATGAGCAATCCGCGCATCTGCGCGCATAGGGCA	338	
DB	883	AGGAAGAAGTAAACATCTCAGCGCGGTGAGACGATCCGCGCACCGCCACCGGAGCGGTA	824	
QY	339	GGCAATATCCGGTGAACGGGGTGGAAACAGCCCTTGGCCCCCAACCGCACCGGACCGCCCT	398	
DB	823	GGGAGTACCCGGTGTCTGCAATGAAACACCCCGCGCGTAACTCGTACAGGCTTTCGGTT	764	
QY	399	GCGGCTGTGCGCGCAGAAAGCCTTAAGGGTCAATGAGCGCCAGCGCGAATGGGCAAGATGCCCC	458	
DB	763	GC-TGTTGCCAAAACCTGACATTAATGCGCCGTTAAACGTAATGGGCAATGACACCTGTTT-	706	
QY	459	TTTCCGCGCGCATCTCTGCCCGGTGCGACGCCCGCGCTGAGCGCATAGTCCAGCGACGCT	518	
DB	705	-TTCCCGGAGCAAGTCTGTAAACGGCCCAACCTGTGTGCGCAGCATTAATCGCAATGTTCT	647	
QY	519	GCGCCAGCGCGCCATGCTCCAGATGCGCGCGGTGCTGTAGCGGCTATCTTCATCAGCA	578	
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DB	586	GTGCGGTTTGGAAAACCGGCAAGGGTATTAACAAACCGGTAGCCATTTTGTCTGATGACCG	527	
QY	639	TGCGGTCATGATCATCGGCGGCTCGACGCGCATGAGGGGGCGGTGCGTCTGCATCTCGACGC	698	
DB	526	TGCAATCATATAATCGGTGACATTAACATAGCGGGCGGCTCAGTTGCCATCTCTGAC	467	
QY	699	CCACGAATTTTGGAAACCAACGCGTCAGGTGCGGGGTTCGACGCGCACCAAGGCGGTGCA	758	
DB	466	CGATTAATAGCTTGGAATCTCTACGGGTATGACGAATCAGGGGTGTAACCCCGTCCGTGCA	407	
QY	759	TCAGCAGGACGCTCCATCCGCGAGCGGTCCGTACAGGTGCGCGCGGATATGTCTCAGG	818	
DB	406	TCCTGTACTGTGGCAATGAATTAATCCGGCCATCCGCTAACCTGGAACCGATTTCAGATTAACG	347	
QY	819	TCGCGACATGGGTATTCACACGCGAGATGACACCTTGACAGACCGCGATACAGCGG---	874	
DB	346	CTGAACCGCGGTATGACGCCATTAATTTGTCCAACTGTTGGCGGAGTATCCCGGCGA	287	
QY	875	-----CCGCGCTCGATCGAGCCATAGCCTGTCTGTCAGCGCGCGCGAATGTGCGGAAAACG	929	
DB	286	AATGCGGGAGGTACACGCAATAGTAGCACACTGTTTCAATGCGGAACGGGTTTGGGGAAAC	227	
QY	930	CGACTCTCTAATCCGTCCATTCGCGCGACGAATAGGTGGACAGGCGCGCCACCACTTTCG	989	
DB	226	GAACCTGTGTATCGGGCCAGTATGAAACACAGGCGGCTATTCAGCGATGCTGATTTCA	167	

D	b		406	TCACCTGTA	TGGCAGAA	TAAATCCGGGCATCCGGTA	ACTGGACCGAATTCAGCAATGAACGG	347					
O	y		819	TCGGACA	TGCGTATT	CCACCGCAGATGACACCCTG	CAGACGCCCATCAGCGG----	874					
D	b		346	CTGAAC	CCGCGGTATG	CAGCCATAAATGTTTGCCA	AATCTGTTGCGGAGTATCCCGCGCA	287					
O	y		875	-----	CCCCCT	CGATCGAGCCATPAG	CCCTGTGTCAAGCGCGCGGAATATGTGCGGAAACG	929					
D	b		286	AATGCC	GGAAGGTCA	CGCAGTAGTAGCAC	TGTTTCAATGCGACGCGGTTGGGGAAC	227					
O	y		930	CGACCT	CTGTATCCG	TTCATTGCGCGCAGCAAA	TGGGCGAACAGCGCCAGCCATTGCG	989					
D	b		226	GAACCT	GTTAGTAC	TGCGGCCAGTAGGACACCA	AGGCGGCTATATCAGGAGATGCTGATTCA	167					
O	y		990	GCGAA	AGAATCCG	TGTCTGTGGACAGACCA	AGTGTCGTGTGTCGAAGGAGCGGACCGCGGT	1049					
D	b		166	GCGTTA	ATATCTCT	CTTCGTGAAGAAGCA	CGAGTATGTTGTTCCCTTCGCGCTCAGAGACCGGCT	107					
O	y		1050	CGAGCA	TATACGATGG	CGGCATTCGGTCTGCGGTG	CGCGAACGGCAAGCCGATCAGCGAC	1109					
D	b		106	CAATA	PAGAAATCCG	CATATCCGATGCTGTGTGA	AGCGGACGCGCATTAAGGCAT	47					
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D	b		46	TAGCC	AGACCGGCAC	CGACGACGAATG	AGATCATAG	12					
RESULT 15													
ID		ADQ77203/c		standard; DNA; 1149 BP.									
XX		ADQ77203;											
XX		23-SEP-2004	(first entry)										
DE		Nucleotide sequence of Pantoea stewartii CrtY protein.											
XX													
KW		carotenoid; carotenoid enzymatic biosynthetic pathway; dks gene;											
KM		D-1-deoxyxylulose 5-phosphate gene; idi gene; ygbp gene; ispB gene;											
KM		yJr gene; oligo-ribonuclease gene; dks gene; dxr gene;											
KM		DOXP reductoisomerase; YgpF gene; ispD gene; ycbB gene; ispE gene;											
KM		ygbB gene; ispF gene; lytB gene; ispH gene; idi gene;											
KM		isopentenyl diphosphate isomerase; ispA gene;											
KM		farnesyl pyrophosphate synthase; ispB gene;											
KM		octaprenyl diphosphate synthase; crtB gene;											
KM		geranylgeranyl pyrophosphate synthase; crtB gene; phytoene synthase;											
KM		crtl gene; phytoene dehydrogenase; crtX gene;											
KM		zeaxanthin glucosyl transferase; crtZ gene; beta-carotene hydroxylase;											
KM		crtY gene; lycopene cyclase; enzyme; gene; ds.											
XX		Pantoea stewartii.											
OS													
XX													
FH		Key	Location/Qualifiers										
FT		CDS	1..1149										
FT			/tag= a										
FT			/product= "CrtY protein"										
XX													
PN		MO2004056975-A2.											
PD													
XX		08-JUL-2004.											
XX													
PF		19-DEC-2003; 2003WO-US041812.											
XX													
PR		19-DEC-2002; 2002US-043461BP.											
XX													
PA		(DUPO) DU PONT DE NEMOURS & CO E I.											

PT Flavobacterium, comprising genes encoding functional carotenoid enzymatic
 PT biosynthetic pathway, useful for producing carotenoids such as
 PT astaxanthin and beta-carotene.
 PS
 XX
 XX
 XX
 CC The specification describes a carotenoid overproducing bacteria, which
 CC comprise genes encoding a functional carotenoid enzymatic biosynthetic
 CC pathway, where the dxs (D-1-deoxyxylulose 5-phosphate gene), idi, ygbBP
 CC and isgB genes are overexpressed, and the yler gene (oligo-ribonuclease
 CC gene) is down regulated. In bacteria of the invention, the carotenoid
 CC enzymatic biosynthetic pathway consists of the genes dxs, dxr (DOXP
 CC reductoisomerase), yggp (also known as ispD), ychB (also known as isgB),
 CC ygdB (also known as ispP), lytB (also known as ispI), idi (isopentenyl
 CC diphosphate isomerase), ispA (farnesyl pyrophosphate synthase), ispB
 CC (octaprenyl diphosphate synthase), crtB (geranylgeranyl pyrophosphate
 CC synthase), crtB (phytoene synthase), crtI (phytoene dehydrogenase), crtX
 CC (zeaxanthin glucosyl transferase), crtZ (beta-carotene hydroxylase) and
 CC crtC (lycopene cyclase). The lytB and dxr gene are optionally
 CC overexpressed. Carotenoid overproducing bacteria of the invention are
 CC useful for producing carotenoids. The present sequence encodes a CrtY
 CC protein.
 XX
 XX Sequence 1149 BP; 228 A; 325 C; 315 G; 281 T; 0 U; 0 Other;
 SO

Query Match	18.3%	Score 209.8	DB 12	Length 1159
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QY	222 GCAGAAACGGGTGCGGATTCGCGCGCATCGATGAGGCCAG---CCGCGCACCCGCGCAGCGG	278		
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QY	339 GCGAATATCCGGGTGACGGGGTGGGAACAGCCCTGACCCCAAGCCCAACCGGCAACCGGCCCT	398		
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QY	399 GCGCGTGTGCGCGCAGAGGCTTATGCGGTATATGGGCCAGCGCGATGGGACAGATGCCCC	458		
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Db	646 GACCGCGCGCTTCCGCGCTGAAGATTAGCTTGTCAATGATGATGTGCTTTGATCAAGA	587		
QY	579 TGCGGGTGGACTGAAGGCGACAGATATGATGAAGCGGTATCCGTTCACTTGGGACCG	638		
Db	586 GTGCGGTTCGGAAGCGCGCAGGGTATTAACAAAGCGGTAGCCATTTTGTCTGATGACCG	527		
QY	639 TGGGTGCATATATATGGGGGCTCGAAGCCATGGGGGGCGGTCCGATCTCGATCTGACGC	698		
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QY 930 CGACCTCTGATCCGTCATTGCGCGGACGAATGGGCGACAGCGCGCCAGCCATTGCG 989
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Search completed: June 21, 2005, 20:32:40
Job time : 756.928 secs

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DB 849 CGCGGATGATGACCCAGCCGCGACCGCGGACGCGGATGTCAGTCCG 790
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DB 789 GAACAGCCCTGCCCCAGCCGCGACCGCGGATGTCAGTCCG 730
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RESULT 2
LOCUS A84704 1149 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 14 from Patent EP0872554.
ACCESSION A84704
VERSION A84704.1 GI:6733573
KEYWORDS

SOURCE unidentifed
ORGANISM unidentifed
REFERENCE 1 (bases 1 to 1149)
AUTHORS Paramontes, L. and Teygankov, Y. S.
TITLE Improved fermentative carotenoid production
JOURNAL Patent: EP 0872554-A 14 21-OCT-1998;
HOFMANN LA ROCHE (CH)
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.5e-141;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1089 AATGCGCGGCGGTCTGCTGAGATGCGAAGCCGCTCGGCAATGTCAGGCGCGGCTA 1030
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LOCUS ARI03082
DEFINITION Sequence 8 from patent US 6087152.
ACCESSION ARI03082
VERSION ARI03082.1 GI:12814670
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1149)
AUTHORS Hohmann,H.-P., Pasamontes,L., Tessier,M. and van Loon,A.
TITLE Fermentative carotenoid production
JOURNAL Patent: US 6087152-A 8 11-JUL-2000;
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ORIGIN

Query Match 100.0%; Score 1149; DB 6; Length 1149;

Best Local Similarity 100.0%; Pred. No. 3.5e-141; Mismatches 0; Indels 0; Gaps 0;

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Db 1089 AATGGCGCGCGCGTCCGCGTACGATGCGAAGCGCGTGGCGCAATGATAGGCGCCCGGCATA 1030
QY 121 GAAGCGCTGATCAGCGGCTGCGGCGAGGCGGTAGAACCGCTGCGACGAGCGATAGCGAGC 180
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QY 181 GTGCGCGCGCGCGCGCGGACAGCATTCGGGTTTCAGACGCGCGAGAGAGCGGTTCGATC 240
Db 969 GTGCGCGCGCGCGCGCGGACAGCATTCGGGTTTCAGACGCGCGAGAGAGCGGTTCGATC 910
QY 241 CGCGCATGATGAGCGCGCGCGCGACCGCGCGAGCGGCGGAGACGCGGTTCGATCAGTCCGCG 300
Db 909 CGCGCATGATGAGCGCGCGCGCGACCGCGCGAGCGGCGGAGACGCGGTTCGATCAGTCCGCG 850
QY 301 CGCGCATGATGAGCGCGCGCGCGCTGCGCGGATGAGGCGAGCGATATCCGCTGACGCGGCTG 360

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RESULT 4
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LOCUS ARI39698
DEFINITION Sequence 8 from patent US 6207409.
ACCESSION ARI39698
VERSION ARI39698.1 GI:14482194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1149)
AUTHORS Hohmann,H.-P., Pasamontes,L., Tessier,M. and van Loon,A.
TITLE Fermentative carotenoid production
JOURNAL Patent: US 6207409-A 8 27-MAR-2001;

QY 481 GGTCCAGCCCGCTGCGGCATATGTCAGCGACGCGCTGCGCAGCGCCCAATCGTCCAG 540
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DEFINITION Flavobacterium ATCC21588 geranylgeranyl synthase (crtB), phycoene synthase (crtI), phycoene desaturase (crtI), lycopen cyclase (crtY), b-carotene hydroxylase (crtZ) genes, complete cds.
ACCESSION U62808
VERSION U62808.1 GI:1842241
KEYWORDS Flavobacterium sp. ATCC 21588
SOURCE Flavobacterium sp. ATCC 21588
ORGANISM Bacteria; Bacteroidetes; Flavobacteriales; Flavobacteriales; Flavobacteriaceae; Flavobacterium.
REFERENCE 1 (bases 1 to 5188)
AUTHORS Pasamontes, L., Hug, D., Tessier, M., Hohmann, H. P., Schierle, J. and van Loom, A. P.
TITLE Isolation and characterization of the carotenoid biosynthesis genes of Flavobacterium sp. strain R1534
JOURNAL Gene 185 (1), 35-41 (1997)
MEDLINE 97186694
PUBMED 9034310
REFERENCE 2 (bases 1 to 5188)
AUTHORS Pasamontes, L.

TITLE Direct Submission
JOURNAL Submitted (03-JUN-1996) VFGB, F. Hoffmann-La Roche Ltd., Basel, 4070, Switzerland
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ACCESSION	AR169831
VERSION	AR169831.1 GI:17907751
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SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 8625)
TITLE	Paasamontes,L. and Teygankov,Y.
JOURNAL	Fermentative carotenoid production
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Best Local Similarity	100.0%; Pred. No. 1.8e-141;
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ACCESSION AR452005
VERSION AR452005.1 GI:42683332
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8625)
AUTHORS Paramotes, L. and Tsyngankov, Y.
TITLE Fermentative carotenoid production
JOURNAL Patent: US 6677134-A 1 13-JAN-2004;

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VERSION	AR169852.1	GI:17907781	
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 11233)		
TITLE	Paramontes, L. and Tsygankov, Y.		
JOURNAL	Fermentative catenoid production		
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OY	541	ATCCGCCCGCGCTGCTGAGCGCGTATCTTCGATCAGGATGCGGGTGGGACTGAAGGCGAG	600
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Db	7136	CTCGACGCCCATGGGGGGCGTTCGATCTTCGATCTCGACGCCCAAGATTCTTGGAAACCCAC	7195
OY	721	GGTCAAGTGTGGGGGTTCGACCGGACCAAGGGGCTCGATCAAGAGGAGGCTGATTCGG	780
Db	7196	GGTCAAGTGTGGGGGTTCGACCGGACCAAGGGGCTCGATCAAGAGGAGGCTGATTCGG	7255
OY	781	CGACCCGCTCCGTCAGCGCGCGCGGATCTCTCAGCGTCTCGACATGCGATTCCACCG	840
Db	7256	CGACCCGCTCCGTCAGCGCGCGGATCTCTCAGCGTCTCGACATGCGATTCCACCG	7315
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OY	901	CGTCAGAGCGGCGCGAATGCTCGGGGAAACGCGACCTTCCTGATCCGTCATTGCGCGCGACG	960
Db	7376	CGTCAGAGCGGCGCGAATGCTCGGGGAAACGCGACCTTCCTGATCCGTCATTGCGCGCGACG	7435
OY	961	AATGCGCGACAGCGCGCGCGCACCATTTGCGGCGAAAGATCCGCTGTCTGTGGCGAGACAGGT	1020
Db	7436	AATGCGCGACAGCGCGCGCGCACCATTTGCGGCGAAAGATCCGCTGTCTGTGGCGAGACAGGT	7495
OY	1021	GTCGTCGTCGAGGGGGGCGGACCGCGCGGTGAGACATACGATGGCGCATCCGCTTGGCG	1080
Db	7496	GTCGTCGTCGAGGGGGGCGGACCGCGCGGTGAGACATACGATGGCGCATCCGCTTGGCG	7555
OY	1081	GTCGCGAAGCGCAAGCGCGATCAGCGCACCGGACAGCCCGCGCGCGCGATCAGCAATC	1140
Db	7556	GTCGCGAAGCGCAAGCGCGATCAGCGCACCGGACAGCCCGCGCGCGCGATCAGCAATC	7615
OY	1141	ATGCGTCAT 1149	
Db	7616	ATGCGTCAT 7624	

RESULT	10			
AR452026				
LOCUS	AR452026	11233 bp	DNA	linear
DEFINITION	Sequence 27 from patent US 6677134.			PAT 20-FEB-2004
ACCESSION	AR452026			
VERSION	AR452026.1	GI:42683353		
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 11233)			
TITLE	Paramontes, L. and Tsygankov, Y.			
JOURNAL	Fermentative carotenoid production			
FEATURES	Patent: US 6677134-A 27 13-JUN-2004;			
source	Location/Qualifiers			
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Best Local Similarity	100.0%;	Pred. No. 1,7e-141;		
Matches 1149; Conservative	0;	Mismatches	0;	Gaps 0;

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RESULT 11
AX429765/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Agrobacterium aurantiacum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

REFERENCE
1 Misawa,N., Kondo,K., Kajiwara,S. and Yokoyama,A.
Dna strands useful for the synthesis of xanthophylls and the
process for producing the xanthophylls
Patent: EP 1203818-A 5 08-MAY-2002;
KIRIN BEER KAIRUSHIKI KAISHA (JP) ; MARINE BIOTECHNOLOGY INSTITUTE
CO., LTD. (JP)

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ORIGIN
Query Match 55.9%; Score 641.8; DB 6; Length 1161;
Best Local Similarity 73.4%; Pred. No. 7.4e-75;
Matches 852; Conservative 0; Mismatches 297; Indels 12; Gaps 2;

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LOCUS AR041163
DEFINITION Sequence 5 from patent US 5811273.
ACCESSION AR041163
VERSION AR041163.1 GI:5961659
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 1161)
AUTHORS Misawa,N., Kondo,K., Kajiwara,S. and Yokoyama,A.
TITLE DNA strands useful for the synthesis of xanthophylls and the process for producing the xanthophylls

JOURNAL Patent: US 5811273-A 5 22-SEP-1998;
FEATURES Location/Qualifiers
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Best Local Similarity 73.4%; Pred. No. 1e-74;
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QY 241 CGCGCGATCGATGCG 294
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QY 355 GGGGTGGAACAGACCTCTGCCCCAGCCAGCCGCGCCCTGTGGCTGTGCGGCA 414
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Db 21 CAGCAGACGTCATGCGGTCA 2

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ACCESSION AR082017
VERSION AR082017.1 GI:10008743
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1161)
AUTHORS Misawa,N., Kondo,K., Kajiwara,S. and Yokoyama,A.
TITLE DNA strands useful for the synthesis of xanthophylls and the process for producing the xanthophylls
JOURNAL Patent: US 5972690-A 5 26-OCT-1999;
FEATURES
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Location/Qualifiers
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Best Local Similarity 73.4%; Pred. No. 18-74;
Matches 851; Conservative 0; Mismatches 297; Indels 12; Gaps 2;
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Db 681 GCGCGCGGTTCAGCGCGCTTGTGCGCGCGCATATGTCGAGAGCGCGCGCGCGCGCGTGTG 622
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RESULT 14
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DEFINITION beta-Carotene hydroxylase gene and use thereof.
ACCESSION E22378
VERSION E22378.1 GI:13024037
KEYWORDS JP 1999046770-A/2.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1161)
AUTHORS Norihiro,M., Kazumori,M., Kitchi,K. and Hiroyuki,F.
TITLE beta-Carotene hydroxylase gene and use thereof
JOURNAL Patent: JP 1999046770-A 2 23-FEB-1999;
KIRIN BREWERY CO LTD
OS Agrobacterium aurantiacum
PN JP 1999046770-A/2
PD 23-FEB-1999
PF 07-AUG-1997 JP 1997213648
PR NORIHIKO MISAWA,KAZUMORI MASAMOTO,KITACHI KANEKO,HIROYUKI FUJI

	PC	C12N15/09, C12N1/19, C12N1/21, C12N5/10, C12P23/00// (C12N15/09, P
	PC	(C12N15/09)
	PC	(C12N15/09, C12R1:01), (C12N15/09, C12R1:18), (C12N1/21, C12R1:19),
	PC	(C12P23/00, C12R1:19), C12N15/00, C12N5/00, C12N15/00, C12R1:89),
	PC	(C12N15/00, C12R1:01), (C12N15/00, C12R1:18)
	CC	Strandedness: Double;
	CC	Topology: Linear;
	FH	Key
	FT	source
	FT	Location/Qualifiers
	FT	Location/Qualifiers
	FT	/organism='Agrobacterium aurantiacum'.
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		/organism="unidentified"
		/mol_type="genomic DNA"
		/db_xref="taxon:32644"
	ORIGIN	
	Query Match	55.8%; Score 640.8; DB 6; Length 1161;
	Best Local Similarity	73.4%; Pred. No. 1e-74;
	Matches	851; Conservative 0; Mismatches 297; Indels 12; Gaps 2;
Oy	1	TCAATGCTCTTCCTCGACAGAGGGGCGTTCCGGGCAGAGCGACAAGCGCTTCCGACAGCGG 60
Db	1161	TCATGCCGTTTTCTTCCTTAGCAGAGGAGCGATTCCGGGCAGAGCGAGATATGGCGCCAGAGGG 1102
Oy	61	AATGGGCGGGGCGTGCCGGTGAAGATGACAAAGCCGGTCCGGCCAAATGACAGAGCGCCCCGACATA 120
Db	1101	AATGGAGAGGCTTGGCCGGTACAGATGCGAGCTGTATCCGCACCGCTCACGCCGGCCGGCATTA 1042
Oy	121	GAAAGCGCTCATAGTCAGCGGCTCGGCAGAGGCGGTAGAACCCGCTGCAGACAGAGCGGATATGACAG 180
Db	1041	GAAACCGTTGCATCATAGTCATCGATCGGCGATGCGGTAGAACCGCTGCAGACAGCGGATATGACGCG 982
Oy	181	GTCGGGCGGGGAGAGCCCGGGAACAGATATCCGCTTTCAGACAGCCGCAAGAAAGCGGTGCCATC 240
Db	981	GTCGGGCGCGGAGCGCGGAACAGATATCCGCTTCAAAGAAGGCGAAGAAAGCGGTGCGCGCG 922
Oy	241	CGCGCGATCATATGAGGCGCCAGCGCGACCGCGCAGCG-----GGCGGACGCGGCTGCTCAG 294
Db	921	CGCCCGGCTCGATTCGCGTAAATGCGGATATGCGGATATGCGGCGCGCGCGAGCGCGCTGCGCGCGCGCGCC 862
Oy	295	GTCGCGCGCGCGCATGCGATCCGCGACTTCGCGCGCATATGGGCAAGCGAATATCCGCTGAC 354
Db	861	GGAAGAGACCGCCGACCAAGCTCCGCGCACTGTCGCGCATATGGGCAAGCGAATATGCGGCTGAC 802
Oy	355	GGGGTGAAGAACCCCTGCGCCCAAGCCCAACCGGACACCGCCCCCTCGCGGTATGATGCGCCA 414
Db	801	CGGATGAAAAGAACCCCGCGCGCAAGTCCACAGGAAACAGGCCCCCGCGGTATGCGCCA 742
Oy	415	GAAAGCTATGAGCGTCAATGGGCGAGCGCATATGGGCGAGATGCGCCCTTTCGCGCGCATATC 474
Db	741	GAAAGCCCGCCGATCATATGGGCGAGCGCATATGGGAAAGATGCGCGGCTTTCGCGCCGGAATC 682
Oy	475	CTGCCCGGTCAGCCCGCGCTTCGCGGCAATGATCCAGCGCAGCGCTTCGCGCAAGCGCGCATC 534
Db	681	GGCCCGGCTCAGCCCTGCTGCGGCGCATATGTCGTVGGGACCGCCGCGCGCAGCGCGTGC 622
Oy	535	GTCAGATATGCGCGCGCGCTGCTGTAGCGGTATCTTCATATCAGATATGCGGGTGGGACTGAA 594
Db	621	GTCAGATATGCGCGCGCATATGAAATAGCGGTGCTTCATATCAGATATGCGCGTGGAGAGAA 562
Oy	595	GGGAGCAGATATGATGAAGCGGTACC CGGTCAATCGCGGAACGGATCGCGTCCATGATCAT 654
Db	561	GGGAGCAGATATGATGAAGCGGTACCGGTCTTGCTGGGTAGCGATCGGCTTCATGATCAT 502
Oy	655	CGGCGCTCATAGCCCATATGGGGGCGGTGCTTCGATCTGACGCGCCCAAGAAATTTCTGAA 714
Db	501	CGGCGCGGAGCAGCGCGTGGGGGCGGTGCGGTCTCGATCTGACACCCAGAAATTTCTGAAA 442
Oy	715	ACCACAGGTCAAGTTCGGGGTCTTCAGACGGCAACAGGGCGTTCATCAAGCAGAGGACGCTC 774
Db	441	ACCACAGGTCAAGTTCGGCGAGCGGCTGCGCGCCCGCGCTTCAGAAACGGGCGCGGCTC 382

Oy	775	GATCCGGAGGCGCTCCCTCAGCGCTGCGCGGTAATCGTCCAGCGCTCGCATATCGTAAT	834
Db	381	GATCCGGGTGCGGAGGACAGCGTCTGCCCTCGTGCGATTCAGACAGGGGGAATGTCGTCT	322
Oy	835	CCACCGCAGATCGACACCTTCAGACAGC-----CCGATCAGCGCGCCCGCTTCGATCGA	888
Db	321	CCACCGGATCTCGCGCGCCCGACCGAACACCGCATTCGCGCAGCGCGCCCGCTTCAGCGA	262
Oy	889	GGCATTCAGCTGTCTCAGAGGGGCGCGGAATGGTGGGAAACCGCGACTTCGTGATCCGTCCA	948
Db	261	CCCGTAACCGGTGGCCAGCGCGCCGGGCAATGGCGGGGAAAGCGCACTTCCTGTGTGGGCA	202
Oy	949	TTCCCGCGCAGATGAGGGCGACAGCGCGCGCAGCATTCCTGGCGAAGATCCGTGTGTG	1008
Db	201	GTTGGCGCGCGGACAGGGGCTTACCGCGCGCACGATGTCGCGCGACAGGTGGGGTGTG	142
Oy	1009	GCAGAGCACAGGTGTGCTGTGTCCGAGGCGCGCGACCGCGCGTGCAGCATTCAGATCGCGC	1068
Db	141	GCAGAGCACAGGTGTGGCGGTGTGACGGGTCTGCGGCATGTGTCAGACAGCACAGCGCGAG	82
Oy	1069	ATCCGGTCTGTGGGTTCGCGGAACGGACGCGCATTCAGGGCACCGGACAGCCCGCGCCCGC	1128
Db	81	GTCGGCGCGCGCGCGCGCGCGACGCGCGCATCAGCCCGTGTGGCAAGCGCCCGCTGCG	22
Oy	1129	GATCAGCAGATCATGCTGCTCA	1148
Db	21	CAGCAGCACGCTCATGGCTCA	2
RESULT 15			
LOCUS	AR041164/c	2886 bp	DNA
DEFINITION	Sequence 7 from patent US 5811273.		Linear
ACCESSION	AR041164		
VERSION	AR041164.1	GI:5961660	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2886)		
TITLE	Misawa,N., Kondo,K., Kajiwara,S. and Yokoyama,A.		
JOURNAL	DNA strands useful for the synthesis of xanthophylls		
FEATURES	Patent: US 5811273-A 7 22-SEP-1998;		
source	Location/Qualifiers		
	1..2886		
ORIGIN	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	55.8%;	Score 640.8;	DB 6;
Best Local Similarity	73.4%;	Pred. No. 7.4e-75;	
Matches 851,	Conservative % 0;	Mismatches 297;	Indels 12;
		Gaps 2;	
Oy	1	TCATGCTCTCTCTTCGACAGCGGGGCGTTGGGAGAGCAGCGCACCGCTTCGACAGCGG	60
Db	2509	TCATGCGCTTTCCTTCACAGAGGAGACGTTTCGGGAGCAGCGAGTGGCGCTGCGCAAGGGG	2450
Oy	61	AATGGGCGGGCGTCCCGGTGACGATGSCGAAGCGCGGTGCGCCAAATTCAGCGCGCCGGGATA	120
Db	2449	AATGGAGGCGTTCGCGCGGTACAGATGCGCAGCTGATTCGCGCACGCTCAGCGCGCGGATATA	2390
Oy	121	GAACGCTTCGATACAGCGGAGCTTCGGCAGCGGTAAGAACCGCTTCGACAGCGGATAGCAGC	180
Db	2389	GAACCGTTTCATGATCGATCCATCGCGGACATGGGTAGAACCGCTTCGACAGGGATATGCGCG	2330
Oy	181	GTCGGGCGGGCAGCGCGCGGAACAGCATTCGGTTACAGACCGCGCAGGAAGCGGTGGCGATC	240
Db	2329	GTCGGGCGCGGACGCGCGGAACAGCATTCGGTTCAAAAGGCGCGAAGAGCGGTGCGCGC	2270
Oy	241	CGGCGATTCGATGGCGCCAGCGCGGCGCACCGCGCGACG-----GGCGGACGCGGTGTGAG	294
Db	2269	CGCCCGGTTCATCCGTAATGCGGATGGCGCGCGCGCGACGCGGTTCGGTCCGCGCGCGCC	2210

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